

Thu Dec 15 12:21:43 2005

us-10-063-557-50.multi.rag

Blanchard, D.
10/06/3557 Page 1
Seq ID 50

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: December 14, 2005, 06:19:30 ; Search time 121 Seconds
(without alignments)
323.179 Million cell updates/sec

Title: US-10-063-557-50

Perfect score: 461

Sequence: 1 MERVYALLALLAGLTALBAN.....HSPVEKALPITPGSATTC 89
BLOSUN62

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

2443163

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 1500 summaries

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1 ID AAY66705 standard; protein; 89 AA.

DE Membrane-bound protein PRO1069.

PN WO9563088-A2.

PD 09-DEC-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 3; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 2 ID AAY67258 standard; protein; 89 AA.

DE Human signal peptide containing protein HSP-35 SEQ ID NO:35.

PN WO20000610-A2.

PD 06-JAN-2000.

PA (INCY-) INCYTE PHARM INC.

Query Match 100.0%; Score 461; DB 3; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 3 ID AAY65679 standard; protein; 89 AA.

DE Human kidney disease associated protein SEQ ID 11.

PN WO200061622-A2.

PD 19-OCT-2000.

PA (INCY-) INCYTE PHARM INC.

Query Match 100.0%; Score 461; DB 3; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 4 ID AAU29123 standard; protein; 89 AA.

DE Human PRO polypeptide sequence #100.

PN WO200168848-A2.

PD 20-SEP-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 5 ID AAB87550 standard; protein; 89 AA.

DE Human PRO1069.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 6 ID AAB65228 standard; protein; 89 AA.

DE Human PRO1069 (UNQ526) protein sequence SEQ ID NO:262.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 7 ID ABG95875 standard; protein; 89 AA.

DE Human secreted/transmembrane protein PRO1069.

PN US200219130-A1.

PD 29-AUG-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 5; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 8 ID ABUS8499 standard; protein; 89 AA.

DE Human PRO polypeptide #100.

PN US200302727-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 9 ID ABUS8047 standard; protein; 89 AA.

DE Novel human secreted and transmembrane protein PRO1069.

PN US2003032127-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 10 ID ABUS4362 standard; protein; 89 AA.

DE Human secreted/transmembrane protein (PRO) #100.

PN US2003032112-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 11 ID ABR66236 standard; protein; 89 AA.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.

PN US2003027278-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 12 ID ABR65626 standard; protein; 89 AA.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.

PN US2003036159-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 13 ID ABUS9566 standard; protein; 89 AA.

DE Human secreted/transmembrane protein (PRO) #100.

PN US2003040070-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 14 ID ABUS8043 standard; protein; 89 AA.

DE Human PRO polypeptide #75.

PN US2003027163-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 15 ID ABUS9121 standard; protein; 89 AA.

DE Novel human secreted or transmembrane protein PRO1069.

PN US2002132252-A1.

PD 19-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 461; DB 6; Length 89;

Best Local Similarity 100.0%; Pred. No. 4e-50;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 06:27:56 ; Search time 33 Seconds

(without alignments)
222.974 Million cell updates/sec

Perfect score: 461
Sequence: 1 MERVTLALLAGLTALEAN.....HSPVPEKAPLITPGSARTTC 89

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCrus-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	2	US-09-289-349-11
6	276.5	60.0	88	2	US-09-724-864-58
7	256.5	55.6	87	1	US-08-725-531-5
8	256.5	55.6	87	1	US-08-738-127-5
9	256.5	55.6	87	1	US-09-213-392-5
10	256.5	55.6	87	1	US-09-083-661-5
11	214.5	46.5	87	1	US-08-289-247B-4
12	214.5	46.5	87	1	US-08-725-531-4
13	214.5	46.5	87	1	US-08-738-127-4
14	214.5	46.5	87	1	US-09-213-392-4
15	214.5	46.5	87	1	US-09-083-661-4
16	214.5	46.5	124	2	US-09-949-016-8238
17	214.5	46.5	124	2	US-09-949-016-8239
18	191.5	41.5	178	2	US-09-949-016-9028
19	191.5	41.5	178	2	US-09-949-016-9029
20	131	28.4	106	2	US-09-621-976-5338
21	131	28.4	107	2	US-09-621-976-5332
22	129	28.0	92	1	US-08-738-127-1
23	129	28.0	92	1	US-09-247-155-120
24	129	28.0	92	2	US-09-148-545-238
25	129	28.0	92	2	US-09-621-011-238
26	129	28.0	92	2	US-09-903-190-120
27	129	28.0	93	2	US-09-148-545-183
28	129	28.0	93	2	US-09-621-011-183
29	126.5	27.4	92	1	US-08-725-531-3
30	126.5	27.4	92	1	US-08-738-127-3
31	126.5	27.4	92	1	US-09-213-392-3
32	126.5	27.4	92	1	US-09-083-661-3

33	121	26.2	70	2	US-09-148-545-269	Sequence 269, App
34	121	26.2	70	2	US-09-621-011-269	Sequence 269, App
35	112.5	24.4	95	1	US-08-725-531-1	Sequence 1, Appl
36	112.5	24.4	95	1	US-09-213-392-1	Sequence 1, Appl
37	112.5	24.4	95	1	US-09-083-661-1	Sequence 1, Appl
38	112.5	24.4	96	2	US-09-149-476-473	Sequence 473, App
43	106	23.0	69	2	US-09-149-476-606	Sequence 606, App
44	103.5	22.5	95	2	US-09-621-976-5250	Sequence 5250, App
45	99.5	21.6	72	2	US-08-905-223-405	Sequence 405, App
46	94	20.4	179	2	US-09-205-258-424	Sequence 424, App
47	94	20.4	179	2	US-10-004-860-424	Sequence 424, App
48	89	19.3	80	2	US-09-621-976-6085	Sequence 6085, App
49	83	18.0	86	2	US-09-949-016-8419	Sequence 8419, App
50	83	18.0	86	2	US-09-949-016-8420	Sequence 8420, App
51	73.5	15.9	58	1	US-08-725-531-6	Sequence 6, Appl
52	73.5	15.9	58	1	US-08-738-127-6	Sequence 6, Appl
53	73.5	15.9	58	1	US-09-213-392-6	Sequence 6, Appl
54	73.5	15.9	58	1	US-09-083-661-6	Sequence 6, Appl
55	67.5	14.6	664	2	US-09-268-140-2	Sequence 9005, App
56	67.5	14.6	664	2	US-09-949-016-9005	Sequence 10182, App
57	66.5	14.4	376	2	US-09-198-452A-1112	Sequence 10182, App
58	66.5	14.4	388	2	US-09-438-185A-1038	Sequence 6195, App
59	66.5	14.4	523	2	US-09-949-016-6195	Sequence 8164, App
60	66.5	14.4	523	2	US-09-949-016-8164	Sequence 17121, A
61	64.5	14.0	729	2	US-09-248-796A-17121	Sequence 3, Appl
62	63	13.7	627	2	US-10-222-100-3	Sequence 66, Appl
63	62.5	13.6	339	2	US-09-690-454-66	Sequence 174, App
64	62.5	13.6	340	2	US-09-690-454-174	Sequence 7324, App
65	62.5	13.6	389	2	US-09-328-352-7324	Sequence 342, App
66	62	13.4	78	2	US-09-749-637A-942	Sequence 8000, App
67	62	13.4	360	2	US-09-489-039A-8000	Sequence 4, Appl
68	62	13.4	601	2	US-09-336-643A-4	Sequence 3725, App
69	61.5	13.3	103	2	US-09-107-532A-7725	Sequence 925, App
70	61.5	13.3	433	2	US-09-198-452A-825	Sequence 860, App
71	61.5	13.3	433	2	US-09-438-185A-860	Sequence 3, Appl
72	61.5	13.3	549	2	US-09-120-365-3	Sequence 41830, A
73	61.5	13.3	549	2	US-09-515-039-3	Sequence 7, Appl
74	61.5	13.3	606	2	US-09-270-767-41830	Sequence 41830, A
75	61.5	13.3	990	2	US-10-363-937-7	Sequence 7, Appl
76	61	13.2	457	2	US-09-489-039A-12762	Sequence 341, App
77	60.5	13.1	106	2	US-09-149-476-341	Sequence 13, App
78	60.5	13.1	288	2	US-09-386-642-13	Sequence 28424, A
79	60.5	13.1	998	2	US-09-252-991A-28424	Sequence 17625, A
80	60	13.0	234	2	US-09-248-796A-17625	Sequence 2, Appl
81	60	13.0	337	2	US-08-930-830B-2	Sequence 5, Appl
82	60	13.0	342	2	US-09-949-016-7352	Sequence 7352, App
83	60	13.0	404	2	US-09-252-991A-27522	Sequence 1, Appl
84	60	13.0	426	2	US-09-718-693A-1	Sequence 652, App
85	60	13.0	497	2	US-09-227-357-652	Sequence 370, App
86	59	12.8	83	2	US-09-973-278-370	Sequence 4819, App
87	59	12.8	430	2	US-09-134-000C-4819	Sequence 13, App
88	59	12.8	539	1	US-08-464-340A-13	Sequence 13, App
89	59	12.8	806	2	US-09-833-466-13	Sequence 12, Appl
90	59	12.8	854	2	US-09-833-466-12	Sequence 6, Appl
91	59	12.8	858	2	US-09-275-252A-6	Sequence 52285, App
92	59	12.8	142	2	US-09-543-681A-5222	Sequence 27855, A
93	58.5	12.7	200	2	US-09-252-991A-27855	Sequence 4908, App
94	58.5	12.7	243	2	US-09-107-533A-9908	Sequence 7, Appl
95	58.5	12.7	260	2	US-09-070-526-2	Sequence 41, Appl
96	58.5	12.7	260	2	US-09-618-259-7	Sequence 41, Appl
97	58.5	12.7	383	1	US-08-314-596-41	Sequence 41, Appl
98	58.5	12.7	383	1	US-08-320-982-41	Sequence 41, Appl
99	58.5	12.7	383	1	US-08-819-037-41	Sequence 41, Appl
100	58.5	12.7	383	2	US-08-530-862B-6	Sequence 6, Appl
101	58.5	12.7	383	2	US-08-597-311D-6	Sequence 6, Appl
102	58.5	12.7	383	2	US-09-059-769-9	Sequence 14, Appl
103	58.5	12.7	383	2	US-09-161-994A-14	Sequence 41, Appl
104	58.5	12.7	383	2	US-09-045-940-41	Sequence 41, Appl
105	58.5	12.7	383	2	US-09-763-331-4	Sequence 4, Appl
106	58.5	12.7	383	2	US-09-697-379-2	Sequence 2, Appl
107	58.5	12.7	383	2	US-10-116-212A-2	Sequence 2, Appl
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112	58.5	12.7	383	2	US-09-885-189-6	Sequence 6, Appli	185	56	12.1	605	2	US-09-252-991A-24349	Sequence 24349, A
113	58.5	12.7	1058	2	US-09-902-540-19449	Sequence 14949, A	186	56	12.1	1058	2	US-09-949-016-11457	Sequence 11457, A
114	58.5	12.7	1518	2	US-09-489-039A-11177	Sequence 11177, A	187	56	12.1	1384	2	US-08-826-134-2	Sequence 2, Appli
115	58	12.6	427	2	US-09-489-039A-10271	Sequence 10271, A	188	56	12.1	1384	2	US-09-949-016-6395	Sequence 6395, Ap
116	58	12.6	428	2	US-09-902-540-14326	Sequence 14326, A	189	56	12.1	1633	2	US-09-902-540-12892	Sequence 12892, A
117	58	12.6	681	2	US-10-104-047-3586	Sequence 3586, Ap	190	56	12.1	1805	2	US-09-949-016-8246	Sequence 8246, Ap
118	57.5	12.5	27	2	US-09-962-766-1644	Sequence 1644, Ap	191	55.5	12.0	175	2	US-09-252-991A-32945	Sequence 32945, A
119	57.5	12.5	352	2	US-09-252-991A-17455	Sequence 17455, A	192	55.5	12.0	248	1	US-08-313-553-3	Sequence 3, Appli
120	57.5	12.5	471	2	US-09-252-991A-77897	Sequence 27897, A	193	55.5	12.0	248	1	US-08-303-651-2	Sequence 2, Appli
121	57.5	12.5	499	2	US-09-328-352-5145	Sequence 5145, Ap	194	55.5	12.0	248	2	US-08-767-993-3	Sequence 3, Appli
122	57.5	12.5	458	1	US-09-902-540-12205	Sequence 12205, A	195	55.5	12.0	262	2	US-08-313-553-2	Sequence 2, Appli
123	57.5	12.5	429	2	US-08-527-152-2	Sequence 2, Appli	196	55.5	12.0	262	2	US-08-767-993-3	Sequence 2, Appli
124	57.5	12.5	775	2	US-09-252-991A-28461	Sequence 28461, A	197	55.5	12.0	292	1	US-08-555-568B-19	Sequence 19, Appli
125	57.5	12.5	1107	2	US-09-489-039A-8890	Sequence 8890, Ap	198	55.5	12.0	292	2	US-09-519-223-19	Sequence 19, Appli
126	57	12.4	185	2	US-10-018-924-6	Sequence 6, Appli	199	55.5	12.0	292	2	US-09-927-180-19	Sequence 19, Appli
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128	56.5	12.3	89	1	US-07-939-501A-2	Sequence 2, Appli	201	55.5	12.0	384	1	US-08-675-650B-2	Sequence 2, Appli
129	56.5	12.3	89	1	US-07-966-187-5	Sequence 5, Appli	202	55.5	12.0	384	2	US-09-354-221B-14	Sequence 14, Appli
130	56.5	12.3	89	1	US-08-371-121-4	Sequence 4, Appli	203	55.5	12.0	384	2	US-09-354-221B-16	Sequence 16, Appli
131	56.5	12.3	89	2	US-07-927-391-6	Sequence 6, Appli	204	55.5	12.0	384	2	US-09-354-221B-18	Sequence 18, Appli
132	56.5	12.3	89	2	US-08-115-753-15	Sequence 15, Appli	205	55.5	12.0	384	2	US-09-128-602B-14	Sequence 16, Appli
133	56.5	12.3	158	2	US-09-107-532A-6092	Sequence 6092, Ap	206	55.5	12.0	384	2	US-09-128-602B-16	Sequence 18, Appli
134	56.5	12.3	168	2	US-09-898-659-16	Sequence 16, Appli	207	55.5	12.0	384	2	US-09-128-602B-18	Sequence 18, Appli
135	56.5	12.3	205	2	US-08-818-112-80	Sequence 80, Appli	208	55.5	12.0	384	2	US-09-995-287-14	Sequence 14, Appli
136	56.5	12.3	205	2	US-08-818-111-81	Sequence 81, Appli	209	55.5	12.0	384	2	US-09-995-287-16	Sequence 16, Appli
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143	56.5	12.3	213	2	US-08-818-112-76	Sequence 76, Appli	216	55.5	12.0	687	2	US-09-519-223-11	Sequence 21, Appli
144	56.5	12.3	213	2	US-08-818-111-77	Sequence 77, Appli	217	55.5	12.0	687	2	US-09-927-180-21	Sequence 21, Appli
145	56.5	12.3	233	2	US-09-056-556-76	Sequence 76, Appli	218	55.5	12.0	688	1	US-08-555-568B-23	Sequence 23, Appli
146	56.5	12.3	233	2	US-09-072-967-77	Sequence 77, Appli	219	55.5	12.0	688	2	US-09-519-223-23	Sequence 23, Appli
147	56.5	12.3	233	2	US-09-072-967-76	Sequence 76, Appli	220	55.5	12.0	688	2	US-09-927-180-23	Sequence 23, Appli
148	56.5	12.3	233	2	US-10-193-002-77	Sequence 77, Appli	221	55.5	12.0	819	2	US-09-949-016-10948	Sequence 10948, A
149	56.5	12.3	233	2	US-10-084-843-76	Sequence 76, Appli	222	55.5	12.0	887	2	US-09-077-940A-2	Sequence 2, Appli
150	56.5	12.3	260	2	US-09-008-271A-7	Sequence 7, Appli	223	55.5	12.0	888	2	US-09-077-940A-4	Sequence 4, Appli
151	56.5	12.3	260	2	US-09-968-415-7	Sequence 3, Appli	224	55.5	12.0	968	2	US-09-228-986-76	Sequence 76, Appli
152	56.5	12.3	385	1	US-08-416-756A-3	Sequence 3, Appli	225	55.5	12.0	968	2	US-10-101-464A-76	Sequence 76, Appli
153	56.5	12.3	385	2	US-08-880-865-3	Sequence 2, Appli	226	55	11.9	124	2	US-09-270-767-33906	Sequence 33906, A
154	56.5	12.3	419	2	US-08-115-753-2	Sequence 3, Appli	227	55	11.9	124	2	US-09-270-767-49123	Sequence 49123, A
155	56.5	12.3	419	2	US-08-115-753-33	Sequence 33, Appli	228	55	11.9	205	2	US-09-248-796A-15224	Sequence 39, Appli
156	56.5	12.3	601	2	US-09-949-016-9977	Sequence 9977, Ap	229	55	11.9	232	1	US-08-456-670B-39	Sequence 39, Appli
157	56.5	12.3	626	2	US-09-957-187-83	Sequence 83, Appli	230	55	11.9	232	1	US-09-372-036-39	Sequence 37, Appli
158	56.5	12.3	630	2	US-09-520-781-30	Sequence 30, Appli	231	55	11.9	359	2	US-09-248-796A-18202	Sequence 42, Appli
159	56.5	12.3	630	2	US-09-957-187-30	Sequence 30, Appli	232	55	11.9	375	2	US-09-103-311-42	Sequence 42, Appli
160	56.5	12.3	630	2	US-09-991-053-30	Sequence 30, Appli	233	55	11.9	376	2	US-09-631-584-51	Sequence 51, Appli
161	56.5	12.3	697	2	US-10-101-464A-940	Sequence 940, App	234	55	11.9	381	2	US-09-248-796A-19630	Sequence 19630, A
162	56.5	12.3	757	2	US-09-949-016-7121	Sequence 7121, Ap	235	55	11.9	404	2	US-09-538-092-50	Sequence 50, Appli
163	56.5	12.3	852	1	US-08-190-802A-67	Sequence 67, Appli	236	55	11.9	406	2	US-09-252-991A-20630	Sequence 20630, A
164	56.5	12.3	852	1	US-08-190-802A-67	Sequence 67, Appli	237	55	11.9	459	2	US-08-311-731A-47	Sequence 47, Appli
165	56.5	12.3	852	2	US-08-477-346-59	Sequence 59, Appli	238	55	11.9	478	1	US-08-456-670B-40	Sequence 40, Appli
166	56.5	12.3	852	2	US-08-477-346-67	Sequence 67, Appli	239	55	11.9	478	1	US-08-372-036-40	Sequence 40, Appli
167	56.5	12.3	852	2	US-08-473-089-59	Sequence 59, Appli	240	55	11.9	484	1	US-08-127-499A-26	Sequence 26, Appli
168	56.5	12.3	852	2	US-08-473-089-67	Sequence 67, Appli	241	55	11.9	484	1	US-08-482-847-26	Sequence 26, Appli
169	56.5	12.3	852	2	US-08-487-072A-59	Sequence 59, Appli	242	55	11.9	512	1	US-08-173-508-4	Sequence 4, Appli
170	56.5	12.3	852	2	US-08-487-072A-67	Sequence 67, Appli	243	55	11.9	512	1	US-08-265-310-4	Sequence 4, Appli
171	56.5	12.3	884	2	US-09-520-781-6	Sequence 6, Appli	244	55	11.9	512	2	US-08-951-742-4	Sequence 4, Appli
172	56.5	12.3	884	2	US-09-957-187-6	Sequence 6, Appli	245	55	11.9	533	2	US-09-549-519-32	Sequence 32, Appli
173	56.5	12.3	884	2	US-09-991-053-6	Sequence 6, Appli	246	55	11.9	598	2	US-09-252-991A-25875	Sequence 25875, A
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175	56.5	12.3	939	2	US-09-957-187-4	Sequence 4, Appli	248	55	11.9	666	1	US-08-346-128-16	Sequence 16, Appli
176	56.5	12.3	939	2	US-09-991-053-4	Sequence 4, Appli	249	55	11.9	666	2	US-08-532-384-17	Sequence 37, Appli
177	56.5	12.3	1030	2	US-09-856-681A-2	Sequence 2, Appli	250	55	11.9	666	2	US-08-616-844-40	Sequence 40, Appli
178	56.5	12.3	1030	2	US-09-856-681A-7	Sequence 7, Appli	251	55	11.9	1481	1	US-08-539-684-40	Sequence 40, Appli
179	56.5	12.3	1047	2	US-09-957-187-85	Sequence 85, Appli	252	55	11.9	1481	1	US-08-944-868A-40	Sequence 40, Appli
180	56	12.1	199	2	US-09-543-681A-5720	Sequence 5720, Ap	253	55	11.9	1481	2	US-08-944-433A-40	Sequence 40, Appli
181	56	12.1	202	2	US-09-489-039A-8619	Sequence 8619, Ap	254	55	11.9	1481	2	US-08-944-433A-40	Sequence 40, Appli
182	56	12.1	316	2	US-09-540-236-3467	Sequence 3467, Ap	255	54.5	11.8	102	2	US-09-540-236-2816	Sequence 2816, Ap
183	56	12.1	579	2	US-09-540-236-2071	Sequence 2071, Ap	256	54.5	11.8	139	2	US-09-270-767-2364	Sequence 2364, Ap
184	56	12.1	593	2	US-09-949-016-10355	Sequence 10355, A	257	54.5	11.8	139	2	US-09-270-767-47581	Sequence 47581, A

258	54.5	11.8	221	2	US-09-270-767-31937	Sequence 31937, A	331	54	11.7	417	4	PCT-US94-07280-19	Sequence 19, Appl
259	54.5	11.8	221	2	US-09-270-767-47154	Sequence 47154, A	332	54	11.7	417	4	PCT-US95-01087-19	Sequence 19, Appl
260	54.5	11.8	220	2	US-09-902-540-11028	Sequence 11028, A	333	54	11.7	434	1	US-08-188-281B-10	Sequence 10, Appl
261	54.5	11.8	251	2	US-08-875-811-59	Sequence 59, Appl	334	54	11.7	434	4	PCT-US94-07280-10	Sequence 10, Appl
262	54.5	11.8	267	2	US-09-634-238-278	Sequence 278, Appl	335	54	11.7	434	4	PCT-US95-01087-10	Sequence 10, Appl
263	54.5	11.8	384	1	US-08-675-650B-4	Sequence 4, Appl	336	54	11.7	441	1	US-08-188-281B-11	Sequence 21, Appl
264	54.5	11.8	384	1	US-08-675-650B-6	Sequence 6, Appl	337	54	11.7	441	4	PCT-US94-07280-21	Sequence 21, Appl
265	54.5	11.8	384	2	US-08-907-608-2	Sequence 2, Appl	338	54	11.7	441	4	PCT-US95-01087-21	Sequence 21, Appl
266	54.5	11.8	384	2	US-08-907-608-4	Sequence 4, Appl	339	54	11.7	443	2	US-09-461-325-147	Sequence 147, Appl
267	54.5	11.8	384	2	US-09-059-759-10	Sequence 10, Appl	340	54	11.7	443	2	US-10-012-542-147	Sequence 147, Appl
268	54.5	11.8	384	2	US-09-354-231B-2	Sequence 2, Appl	341	54	11.7	443	2	US-10-115-123-117	Sequence 147, Appl
269	54.5	11.8	384	2	US-09-354-231B-4	Sequence 4, Appl	342	54	11.7	447	1	US-08-188-281B-20	Sequence 20, Appl
270	54.5	11.8	384	2	US-09-128-602B-2	Sequence 2, Appl	343	54	11.7	447	4	PCT-US94-07280-20	Sequence 20, Appl
271	54.5	11.8	384	2	US-09-128-602B-4	Sequence 4, Appl	344	54	11.7	447	4	PCT-US95-01087-20	Sequence 20, Appl
272	54.5	11.8	384	2	US-09-482-287-2	Sequence 2, Appl	345	54	11.7	453	1	US-08-188-281B-16	Sequence 16, Appl
273	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appl	346	54	11.7	453	4	PCT-US94-07280-16	Sequence 16, Appl
274	54.5	11.8	384	2	US-09-966-888-2	Sequence 2, Appl	347	54	11.7	453	4	PCT-US95-01087-16	Sequence 16, Appl
275	54.5	11.8	384	2	US-09-966-888-4	Sequence 4, Appl	348	54	11.7	458	2	US-09-489-039A-7367	Sequence 7367, Appl
276	54.5	11.8	384	2	US-09-995-297-2	Sequence 2, Appl	349	54	11.7	490	1	US-08-188-281B-15	Sequence 15, Appl
277	54.5	11.8	384	2	US-09-995-297-4	Sequence 4, Appl	350	54	11.7	490	4	PCT-US94-07280-15	Sequence 15, Appl
278	54.5	11.8	426	2	US-09-902-540-12332	Sequence 12332, A	351	54	11.7	490	4	PCT-US95-01087-15	Sequence 15, Appl
279	54.5	11.8	446	2	US-09-543-681A-5864	Sequence 5864, Ap	352	54	11.7	493	2	US-09-170-98A-2	Sequence 2, Appl
280	54.5	11.8	477	2	US-09-489-039A-10570	Sequence 10570, A	353	54	11.7	518	2	US-09-540-235-3648	Sequence 3648, Ap
281	54.5	11.8	481	2	US-09-724-623-77	Sequence 77, Appl	354	54	11.7	880	2	US-09-538-092-601	Sequence 601, Appl
282	54.5	11.8	613	2	US-09-328-352-7962	Sequence 7962, Ap	355	54	11.7	891	2	US-09-252-991A-28689	Sequence 28689, A
283	54.5	11.8	752	1	US-08-281-193-2	Sequence 6860, Ap	356	54	11.7	1036	2	US-09-902-540-14218	Sequence 14218, A
284	54.5	11.8	752	1	US-08-422-106-2	Sequence 2, Appl	357	54	11.7	1623	2	US-09-341-461-2	Sequence 2, Appl
285	54.5	11.8	752	1	US-08-735-716-2	Sequence 2, Appl	358	53.5	11.6	72	2	US-09-188-930-182	Sequence 182, Appl
286	54.5	11.8	752	1	US-08-555-568B-2	Sequence 2, Appl	359	53.5	11.6	221	2	US-09-464-535-22	Sequence 22, Appl
287	54.5	11.8	752	2	US-09-519-223-2	Sequence 2, Appl	360	53.5	11.6	244	1	US-08-361-395-1	Sequence 1, Appl
288	54.5	11.8	752	2	US-09-927-180-2	Sequence 2, Appl	361	53.5	11.6	244	1	US-09-618-259-11	Sequence 11, Appl
289	54.5	11.8	752	4	PCT-US95-08069-2	Sequence 2, Appl	362	53.5	11.6	272	2	US-09-583-110-3866	Sequence 3866, Ap
290	54.5	11.8	765	2	US-09-949-016-7844	Sequence 7844, Ap	363	53.5	11.6	284	2	US-09-902-540-16417	Sequence 16417, A
291	54.5	11.8	780	2	US-09-902-540-10063	Sequence 10063, A	364	53.5	11.6	302	2	US-09-252-991A-21655	Sequence 21655, A
292	54.5	11.8	895	1	US-08-123-161A-8	Sequence 8, Appl	365	53.5	11.6	308	2	US-09-489-039A-14278	Sequence 14278, A
293	54.5	11.8	895	1	US-08-483-278-8	Sequence 8, Appl	366	53.5	11.6	310	2	US-09-107-433-4601	Sequence 4601, Ap
294	54.5	11.8	895	2	US-09-949-016-6490	Sequence 6490, Ap	367	53.5	11.6	325	2	US-09-949-016-7713	Sequence 7713, Ap
295	54.5	11.8	895	2	US-08-949-016-7178	Sequence 7178, Ap	368	53.5	11.6	359	2	US-08-637-670-37	Sequence 37, Appl
296	54	11.7	135	1	US-08-188-281B-6	Sequence 6, Appl	369	53.5	11.6	407	2	US-09-489-039A-13666	Sequence 13666, A
297	54	11.7	135	1	PCT-US94-07280-6	Sequence 6, Appl	370	53.5	11.6	410	1	US-08-723-415B-10	Sequence 1578, Ap
298	54	11.7	135	1	PCT-US95-01087-6	Sequence 6, Appl	371	53.5	11.6	410	1	US-09-189-627A-10	Sequence 10, Appl
299	54	11.7	172	1	US-08-188-281B-5	Sequence 5, Appl	372	53.5	11.6	410	2	US-09-710-861-10	Sequence 10, Appl
300	54	11.7	172	4	PCT-US94-07280-5	Sequence 5, Appl	373	53.5	11.6	415	2	US-09-949-016-8808	Sequence 8808, Ap
301	54	11.7	172	4	PCT-US95-01087-5	Sequence 5, Appl	374	53.5	11.6	437	2	US-09-350-841A-1591	Sequence 1591, Ap
302	54	11.7	172	4	PCT-US94-07280-5	Sequence 5, Appl	375	53.5	11.6	437	2	US-08-486-099-105	Sequence 105, Appl
303	54	11.7	178	2	US-09-936-588-42	Sequence 42, Appl	376	53.5	11.6	438	2	US-08-360-107A-115	Sequence 115, Appl
304	54	11.7	221	4	PCT-US94-07280-2	Sequence 2, Appl	377	53.5	11.6	438	2	US-08-484-741-105	Sequence 105, Appl
305	54	11.7	221	4	PCT-US95-01087-2	Sequence 2, Appl	378	53.5	11.6	438	2	US-08-475-668A-105	Sequence 105, Appl
306	54	11.7	221	4	PCT-US94-07280-2	Sequence 2, Appl	379	53.5	11.6	438	2	US-08-485-551A-105	Sequence 105, Appl
307	54	11.7	221	2	US-09-005-298-46	Sequence 46, Appl	380	53.5	11.6	438	2	US-08-471-913A-105	Sequence 105, Appl
308	54	11.7	241	2	US-08-768-619-46	Sequence 46, Appl	381	53.5	11.6	438	2	US-08-485-264A-105	Sequence 105, Appl
309	54	11.7	346	2	US-09-702-705-329	Sequence 329, Appl	382	53.5	11.6	438	2	US-08-474-349A-105	Sequence 105, Appl
310	54	11.7	346	2	US-09-736-457-329	Sequence 329, Appl	383	53.5	11.6	438	2	US-08-470-896-105	Sequence 105, Appl
311	54	11.7	346	2	US-09-614-124B-329	Sequence 329, Appl	384	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
312	54	11.7	346	2	US-09-589-184-329	Sequence 329, Appl	385	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
313	54	11.7	346	2	US-09-658-824-329	Sequence 329, Appl	386	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
314	54	11.7	346	2	US-10-017-754-329	Sequence 329, Appl	387	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
315	54	11.7	346	2	US-09-519-642-329	Sequence 329, Appl	388	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
316	54	11.7	346	2	US-09-519-642-329	Sequence 329, Appl	389	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
317	54	11.7	346	2	US-09-519-642-329	Sequence 329, Appl	390	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
318	54	11.7	346	2	US-09-519-642-329	Sequence 329, Appl	391	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
319	54	11.7	377	1	US-08-188-281B-17	Sequence 17, Appl	392	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
320	54	11.7	377	4	PCT-US94-07280-17	Sequence 17, Appl	393	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
321	54	11.7	377	4	PCT-US95-01087-17	Sequence 17, Appl	394	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
322	54	11.7	395	2	US-09-540-236-2520	Sequence 2520, Ap	395	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
323	54	11.7	397	1	US-08-188-281B-11	Sequence 11, Appl	396	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
324	54	11.7	397	4	PCT-US94-07280-11	Sequence 11, Appl	397	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
325	54	11.7	397	4	PCT-US95-01087-11	Sequence 11, Appl	398	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, Appl
326	54	11.7	410	1	US-08-188-281B-18	Sequence 18, Appl	399	53	11.5	78	2	US-09-243-675-3	Sequence 3, Appl
327	54	11.7	410	4	PCT-US94-07280-18	Sequence 18, Appl	400	53	11.5	165	2	US-10-104-041-2538	Sequence 2538, Ap
328	54	11.7	410	4	PCT-US95-01087-18	Sequence 18, Appl	401	53	11.5	165	2	US-09-605-703B-2326	Sequence 2326, Ap
329	54	11.7	412	2	US-09-489-039A-9118	Sequence 9118, Ap	402	53	11.5	225	2	US-09-543-681A-4579	Sequence 4579, Ap
330	54	11.7	417	1	US-08-188-281B-19	Sequence 19, Appl	403	53	11.5	239	2	US-08-913-014A-2	Sequence 2, Appl

404	53	11.5	239	2	US-09-653-285-2	Sequence 2, Appli	477	52.5	11.4	410	1	US-08-428-131-2	Sequence 2, Appli
405	53	11.5	299	2	US-09-252-991A-24215	Sequence 24215, A	478	52.5	11.4	410	1	US-08-602-846-2	Sequence 2, Appli
406	53	11.5	319	2	US-09-134-000C-6061	Sequence 6061, Ap	479	52.5	11.4	410	2	US-09-078-596-2	Sequence 2, Appli
407	53	11.5	348	2	US-09-134-001C-4857	Sequence 4857, Ap	480	52.5	11.4	410	2	US-09-189-661-11	Sequence 11, Appli
408	53	11.5	355	2	US-09-902-540-14706	Sequence 14706, A	481	52.5	11.4	410	2	US-09-710-861-11	Sequence 11, Appli
409	53	11.5	356	2	US-09-664-840-2	Sequence 2, Appli	482	52.5	11.4	435	2	US-09-489-039A-13740	Sequence 13740, A
410	53	11.5	377	1	US-08-188-277B-4	Sequence 4, Appli	483	52.5	11.4	448	2	US-09-328-352-5807	Sequence 5807, Ap
411	53	11.5	377	1	US-08-429-964-78	Sequence 78, Appli	484	52.5	11.4	468	2	US-09-602-787A-612	Sequence 612, Ap
412	53	11.5	377	2	US-09-538-092-1199	Sequence 1199, Ap	485	52.5	11.4	483	2	US-09-949-016-7773	Sequence 7773, Ap
413	53	11.5	407	2	US-09-489-039A-13350	Sequence 13350, A	486	52.5	11.4	523	2	US-09-538-092-571	Sequence 571, Ap
414	53	11.5	454	2	US-09-949-016-10198	Sequence 10198, A	487	52.5	11.4	525	2	US-08-888-949-16	Sequence 16, Appli
415	53	11.5	454	2	US-09-489-039A-13505	Sequence 13505, A	488	52.5	11.4	525	2	US-08-888-950-16	Sequence 16, Appli
416	53	11.5	469	2	US-09-902-540-12213	Sequence 12213, A	489	52.5	11.4	525	2	US-09-262-758-16	Sequence 16, Appli
417	53	11.5	476	2	US-09-489-039A-10791	Sequence 10791, A	490	52.5	11.4	525	2	US-09-885-876-16	Sequence 16, Appli
418	53	11.5	476	2	US-09-489-039A-12217	Sequence 12217, A	491	52.5	11.4	525	2	US-09-885-876-16	Sequence 16, Appli
419	53	11.5	482	2	US-09-438-185A-356	Sequence 356, App	492	52.5	11.4	525	2	US-09-731-393-16	Sequence 16, Appli
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421	53	11.5	524	2	US-09-549-519-28	Sequence 28, Appli	494	52.5	11.4	550	2	US-09-515-039-1	Sequence 1, Appli
422	53	11.5	563	2	US-09-949-016-8277	Sequence 8277, Ap	495	52.5	11.4	609	2	US-09-107-532A-5110	Sequence 5110, Ap
423	53	11.5	574	2	US-09-248-796A-16849	Sequence 16849, A	496	52.5	11.4	693	2	US-09-949-016-9666	Sequence 9666, Ap
424	53	11.5	580	2	US-09-489-039A-8096	Sequence 8096, Ap	497	52.5	11.4	706	2	US-09-252-991A-25730	Sequence 25730, A
425	53	11.5	605	2	US-09-902-540-12393	Sequence 12393, A	498	52.5	11.4	763	2	US-10-104-047-7766	Sequence 7766, Ap
426	53	11.5	661	2	US-09-540-236-3743	Sequence 3743, Ap	499	52.5	11.4	800	2	US-09-489-039A-10358	Sequence 10358, A
427	53	11.5	678	2	US-09-252-991A-20202	Sequence 20202, A	500	52.5	11.4	801	2	US-09-583-681A-7561	Sequence 7561, Ap
428	53	11.5	686	2	US-09-252-991A-19332	Sequence 19332, A	501	52.5	11.4	969	2	US-09-321-987B-5	Sequence 5, Appli
429	53	11.5	792	2	US-09-995-587A-11	Sequence 11, Appli	502	52.5	11.4	1000	2	US-09-352-159-25	Sequence 25, Appli
430	53	11.5	896	2	US-09-585-858-17	Sequence 17, Appli	503	52.5	11.4	1000	2	US-09-352-168-25	Sequence 25, Appli
431	53	11.5	896	2	US-10-270-878-17	Sequence 17, Appli	504	52.5	11.4	1000	2	US-09-771-045B-25	Sequence 25, Appli
432	53	11.5	1016	2	US-09-252-991A-18914	Sequence 18914, A	505	52.5	11.4	1000	2	US-09-770-564A-25	Sequence 25, Appli
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434	53	11.5	1146	2	US-09-824-734-2	Sequence 2, Appli	507	52.5	11.4	1101	2	US-08-331-625A-52	Sequence 52, Appli
435	53	11.5	1238	2	US-09-904-065-2	Sequence 2, Appli	508	52.5	11.4	1101	2	US-08-331-625A-54	Sequence 54, Appli
436	53	11.5	1238	2	US-09-904-065-14	Sequence 14, Appli	509	52.5	11.4	1101	2	US-09-494-151-52	Sequence 52, Appli
437	53	11.5	1240	1	US-08-680-326-37	Sequence 37, Appli	510	52.5	11.4	1101	2	US-09-494-151-54	Sequence 54, Appli
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439	53	11.5	1240	2	US-09-904-065-15	Sequence 15, Appli	512	52.5	11.4	1101	2	US-09-972-484-54	Sequence 54, Appli
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441	53	11.5	1339	2	US-09-949-016-10448	Sequence 10448, A	514	52.5	11.4	1279	2	US-09-489-039A-13602	Sequence 13602, A
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443	52.5	11.4	21	2	US-09-962-756-592	Sequence 592, App	516	52.5	11.4	1452	2	US-09-494-151-2	Sequence 2, Appli
444	52.5	11.4	71	2	US-09-369-247-79	Sequence 79, Appli	517	52.5	11.4	1452	2	US-09-972-484-2	Sequence 2, Appli
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446	52.5	11.4	126	2	US-08-331-625A-9	Sequence 9, Appli	519	52.5	11.4	1452	4	PCT-US93-0438A-18	Sequence 18, Appli
447	52.5	11.4	126	2	US-08-331-625A-9	Sequence 9, Appli	520	52.5	11.4	1453	1	US-08-308-872B-6	Sequence 6, Appli
448	52.5	11.4	126	2	US-09-494-151-9	Sequence 9, Appli	521	52.5	11.4	2037	2	US-09-306-998-3	Sequence 3, Appli
449	52.5	11.4	126	2	US-09-972-484-9	Sequence 9, Appli	522	52.5	11.4	2046	2	US-09-949-016-9365	Sequence 9365, Ap
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452	52.5	11.4	216	2	US-09-464-535-28	Sequence 28, Appli	525	52	11.3	127	2	US-09-328-352-4209	Sequence 4209, App
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464	52.5	11.4	384	2	US-09-128-602B-8	Sequence 8, Appli	537	52	11.3	260	2	US-09-593-653-36	Sequence 36, Appli
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467	52.5	11.4	384	2	US-09-482-287-6	Sequence 6, Appli	540	52	11.3	262	2	US-09-303-518D-434	Sequence 434, App
468	52.5	11.4	384	2	US-09-966-888-6	Sequence 6, Appli	541	52	11.3	304	2	US-09-248-796A-17580	Sequence 17580, A
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475	52.5	11.4	396	2	US-09-198-452A-147	Sequence 147, App	548	52	11.3	387	2	US-09-593-653-30	Sequence 30, Appli
476	52.5	11.4	410	1	US-08-723-415B-11	Sequence 11, Appli	549	52	11.3	389	2	US-09-252-991A-22112	Sequence 22112, A

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553	52	11.3	419	2	US-09-446-754-6	Sequence 6, Appl	636	51.5	11.2	384	2	US-08-530-862B-4	Sequence 4, Appl
554	52	11.3	419	2	US-09-206-166-2	Sequence 5, Appl	637	51.5	11.2	384	2	US-08-597-333D-4	Sequence 4, Appl
555	52	11.3	419	2	US-09-206-166-5	Sequence 5, Appl	638	51.5	11.2	384	2	US-09-885-189-4	Sequence 4, Appl
556	52	11.3	420	2	US-09-593-653-28	Sequence 28, Appl	639	51.5	11.2	390	1	US-08-416-756A-5	Sequence 5, Appl
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558	52	11.3	433	2	US-09-949-016-7636	Sequence 7636, Ap	641	51.5	11.2	407	2	US-08-753-007A-6	Sequence 6, Appl
559	52	11.3	433	2	US-09-446-754-2	Sequence 2, Appl	642	51.5	11.2	407	2	US-09-398-496-6	Sequence 6, Appl
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561	52	11.3	453	2	US-09-593-653-32	Sequence 32, Appl	644	51.5	11.2	453	2	US-09-540-236-3464	Sequence 3464, Ap
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568	52	11.3	628	2	US-09-602-787A-550	Sequence 550, App	651	51.5	11.2	550	1	US-08-348-891A-5	Sequence 5, Appl
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571	52	11.3	1194	2	US-09-949-016-9803	Sequence 9803, Ap	654	51.5	11.2	563	2	US-10-046-232-24	Sequence 24, Appl
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576	52	11.3	1957	2	US-08-669-656A-2	Sequence 2, Appl	659	51.5	11.2	707	2	US-10-101-464A-80	Sequence 11, Appl
577	52	11.3	1957	2	US-08-669-656A-8	Sequence 8, Appl	660	51.5	11.2	760	2	US-09-589-892B-11	Sequence 11, Appl
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583	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl	666	51.5	11.2	1454	2	US-09-854-799-32	Sequence 32, Appl
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587	51.5	11.2	123	4	PCT-US94-02629-19	Sequence 19, Appl	670	51.5	11.2	1454	4	PCT-US93-04384-47	Sequence 47, Appl
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592	51.5	11.2	211	2	US-09-603-552-12	Sequence 12, Appl	675	51	11.1	109	2	US-09-438-185A-2	Sequence 2, Appl
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597	51.5	11.2	212	2	US-08-473-326-3	Sequence 3, Appl	680	51	11.1	214	1	US-08-277-231A-14	Sequence 14, Appl
598	51.5	11.2	220	2	US-08-871-572B-13	Sequence 13, Appl	681	51	11.1	214	1	US-08-473-750-3	Sequence 3, Appl
599	51.5	11.2	240	2	US-09-252-991A-30410	Sequence 30410, A	682	51	11.1	214	1	US-08-477-326-3	Sequence 2, Appl
600	51.5	11.2	241	2	US-10-076-069-4	Sequence 4, Appl	683	51	11.1	217	1	US-08-277-231A-2	Sequence 2, Appl
601	51.5	11.2	247	2	US-09-849-016-11579	Sequence 11579, A	684	51	11.1	217	1	US-08-277-231A-12	Sequence 12, Appl
602	51.5	11.2	250	2	US-09-167-717-1	Sequence 1, Appl	685	51	11.1	217	1	US-08-473-750-1	Sequence 1, Appl
603	51.5	11.2	268	2	US-09-818-780-17	Sequence 17, Appl	686	51	11.1	217	1	US-08-473-750-5	Sequence 5, Appl
604	51.5	11.2	268	2	US-09-818-780-94	Sequence 94, Appl	687	51	11.1	217	1	US-08-477-326-1	Sequence 1, Appl
605	51.5	11.2	292	2	US-09-205-258-1116	Sequence 1116, Ap	688	51	11.1	217	1	US-08-477-326-5	Sequence 5, Appl
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607	51.5	11.2	292	2	US-09-107-433-4181	Sequence 4181, Ap	690	51	11.1	230	2	US-09-328-352-7370	Sequence 7370, Ap
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612	51.5	11.2	369	2	US-08-880-865-2	Sequence 2, Appl	695	51	11.1	326	2	US-09-489-039A-11901	Sequence 11901, A
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619	51.5	11.2	381	2	US-09-518-383-18	Sequence 18, Appl	702	51	11.1	354	2	US-09-902-540-15411	Sequence 15411, A
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622	51.5	11.2	382	2	US-09-262-477-2	Sequence 2, Appl	705	51	11.1	365	1	US-08-390-162-2	Sequence 2, Appl
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767	51	11.1	365	2	US-09-949-016-9075	Sequence 9075, Ap	780	50.5	11.0	529	2	US-09-169-717E-39	Sequence 39, Appli
768	51	11.1	370	2	US-09-489-039A-11515	Sequence 11515, A	781	50.5	11.0	529	2	US-10-011-436-4	Sequence 4, Appli
769	51	11.1	380	2	US-09-902-540-15775	Sequence 15775, A	782	50.5	11.0	529	2	US-08-533-895A-39	Sequence 39, Appli
770	51	11.1	383	2	US-08-530-862B-7	Sequence 7, Appli	783	50.5	11.0	537	2	US-08-540-922D-12	Sequence 12, Appli
771	51	11.1	384	2	US-08-597-313D-7	Sequence 7, Appli	784	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appli
772	51	11.1	384	2	US-09-885-189-7	Sequence 7, Appli	785	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appli
773	51	11.1	430	2	US-09-902-540-12684	Sequence 12684, A	786	50.5	11.0	550	1	US-08-279-700-22	Sequence 22, Appli
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775	51	11.1	451	2	US-04-489-039A-8949	Sequence 8949, Ap	788	50.5	11.0	566	2	US-09-491-522-7	Sequence 7, Appli
776	51	11.1	475	2	US-09-489-039A-8862	Sequence 8862, Ap	789	50.5	11.0	566	2	US-09-949-016-7010	Sequence 7010, Ap
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779	51	11.1	490	2	US-09-438-185A-1032	Sequence 1032, Ap	792	50.5	11.0	594	2	US-09-252-991A-22689	Sequence 22689, A
780	51	11.1	534	2	US-09-605-703B-1142	Sequence 1142, Ap	793	50.5	11.0	614	2	US-09-949-016-10772	Sequence 10772, A
781	51	11.1	584	2	US-09-107-532A-4564	Sequence 4564, Ap	794	50.5	11.0	757	2	US-09-902-540-11380	Sequence 11380, A
782	51	11.1	590	2	US-09-248-796A-26874	Sequence 26874, A	795	50.5	11.0	867	2	US-09-839-894-6	Sequence 8, Appli
783	51	11.1	598	2	US-09-248-796A-19180	Sequence 19180, A	796	50.5	11.0	974	2	US-08-938-291A-4	Sequence 4, Appli
784	51	11.1	677	2	US-09-252-991A-30406	Sequence 20406, A	797	50.5	11.0	974	2	US-09-589-619-4	Sequence 4, Appli
785	51	11.1	749	2	US-08-046-508-2	Sequence 2, Appli	798	50.5	11.0	1106	2	US-09-134-000C-6136	Sequence 6136, Ap
786	51	11.1	749	2	US-09-250-083C-2	Sequence 2, Appli	799	50.5	11.0	1163	1	US-08-173-497-4	Sequence 4, Appli
787	51	11.1	822	2	US-09-248-796A-19917	Sequence 19917, A	800	50.5	11.0	1163	1	US-08-286-889-4	Sequence 4, Appli
788	51	11.1	866	1	US-08-386-727-8	Sequence 8, Appli	801	50.5	11.0	1163	1	US-08-485-618-4	Sequence 4, Appli
789	51	11.1	866	1	US-08-600-452A-8	Sequence 8, Appli	802	50.5	11.0	1163	1	US-08-352-552-4	Sequence 4, Appli
790	51	11.1	954	2	US-09-854-845-14	Sequence 14, Appli	803	50.5	11.0	1163	1	US-08-605-672-4	Sequence 4, Appli
791	51	11.1	967	2	US-09-139-802-201	Sequence 201, App	804	50.5	11.0	1163	1	US-08-482-293A-4	Sequence 4, Appli
792	51	11.1	967	2	US-09-659-786-201	Sequence 201, App	805	50.5	11.0	1163	1	US-08-943-363-4	Sequence 4, Appli
793	51	11.1	1049	2	US-09-854-845-2	Sequence 2, Appli	806	50.5	11.0	1163	1	US-08-476-062A-44	Sequence 44, Appli
794	51	11.1	1093	2	US-09-854-845-4	Sequence 4, Appli	807	50.5	11.0	1163	1	US-09-193-043-4	Sequence 4, Appli
795	51	11.1	1151	2	US-09-854-845-10	Sequence 10, Appli	808	50.5	11.0	1163	2	US-09-688-307A-4	Sequence 4, Appli
796	51	11.1	1151	2	US-08-840-062-4	Sequence 10, Appli	809	50.5	11.0	1163	2	US-09-350-259-4	Sequence 4, Appli
797	51	11.1	1479	2	US-08-843-417-10	Sequence 4, Appli	810	50.5	11.0	1163	4	PCT-US96-01314-44	Sequence 44, Appli
798	51	11.1	1956	2	US-09-527-013-10	Sequence 10, Appli	811	50.5	11.0	1211	2	US-09-491-522-5	Sequence 5, Appli
799	51	11.1	26	2	US-09-962-756-1658	Sequence 1658, Ap	812	50.5	11.0	1211	2	US-09-949-016-11401	Sequence 11401, A
800	50.5	11.0	87	2	US-09-605-703B-960	Sequence 960, App	813	50.5	11.0	1211	2	US-09-949-002-601	Sequence 401, App
801	50.5	11.0	87	2	US-09-605-703B-962	Sequence 962, App	814	50.5	11.0	1211	2	US-09-949-002-555	Sequence 555, App
802	50.5	11.0	142	2	US-10-104-047-2706	Sequence 2706, Ap	815	50.5	11.0	1245	2	US-09-252-991A-30935	Sequence 30935, A
803	50.5	11.0	147	2	US-09-543-681A-4506	Sequence 4506, Ap	816	50.5	11.0	1317	2	US-09-083-521-7	Sequence 7, Appli
804	50.5	11.0	188	1	US-08-160-524A-5	Sequence 5, Appli	817	50.5	11.0	1317	1	US-08-185-432-19	Sequence 19, Appli
805	50.5	11.0	207	1	US-08-609-443B-15	Sequence 15, Appli	818	50.5	11.0	2703	2	US-08-899-232-4	Sequence 4, Appli
806	50.5	11.0	207	1	US-08-569-063C-15	Sequence 15, Appli	819	50.5	11.0	2703	2	US-09-121-457-4	Sequence 4, Appli
807	50.5	11.0	207	1	US-08-851-896-15	Sequence 15, Appli	820	50.5	11.0	3169	1	US-08-477-451-6	Sequence 6, Appli
808	50.5	11.0	249	2	US-09-583-110-4357	Sequence 4357, Ap	821	50	10.8	31	2	US-09-270-767-57409	Sequence 31409, A
809	50.5	11.0	249	2	US-09-602-777A-344	Sequence 344, App	822	50	10.8	31	2	US-09-270-767-52626	Sequence 52626, A
810	50.5	11.0	249	2	US-09-107-433-4333	Sequence 4333, Ap	823	50	10.8	69	2	US-09-188-452A-475	Sequence 475, App
811	50.5	11.0	254	2	US-09-605-703B-244	Sequence 244, App	824	50	10.8	92	2	US-09-248-796A-19711	Sequence 19711, A
812	50.5	11.0	263	2	US-09-605-703B-242	Sequence 242, App	825	50	10.8	92	2	US-09-482-273-264	Sequence 264, App
813	50.5	11.0	264	1	US-08-463-115-93	Sequence 93, Appli	826	50	10.8	93	2	US-09-902-540-12546	Sequence 12546, A
814	50.5	11.0	264	1	US-08-463-386-93	Sequence 93, Appli	827	50	10.8	93	2	US-09-543-681A-5280	Sequence 5280, A
815	50.5	11.0	271	2	US-09-252-991A-18965	Sequence 18965, A	828	50	10.8	102	2	US-09-334-142B-16	Sequence 16, Appli
816	50.5	11.0	304	2	US-09-902-540-13553	Sequence 13553, A	829	50	10.8	105	2	US-09-270-767-31650	Sequence 31650, A
817	50.5	11.0	306	2	US-09-252-991A-22181	Sequence 22181, A	830	50	10.8	119	2	US-09-148-452A-266	Sequence 266, App
818	50.5	11.0	326	2	US-09-328-352-5506	Sequence 5506, Ap	831	50	10.8	147	2	US-09-489-039A-12374	Sequence 12374, A
819	50.5	11.0	345	2	US-09-949-016-9786	Sequence 9786, Ap	832	50	10.8	195	2	US-09-303-518D-400	Sequence 400, App
820	50.5	11.0	345	2	US-08-984-618-14	Sequence 14, Appli	833	50	10.8	201	2	US-09-134-000C-6206	Sequence 6206, A
821	50.5	11.0	354	2	US-09-829-275-1	Sequence 2, Appli	834	50	10.8	248	2	US-09-434-238-279	Sequence 279, App
822	50.5	11.0	377	1	US-08-188-277B-2	Sequence 2, Appli	835	50	10.8	252	2	US-09-634-938-479	Sequence 479, App
823	50.5	11.0	377	1	US-08-429-964-80	Sequence 80, Appli	836	50	10.8	252	2	US-09-902-540-12546	Sequence 12546, A
824	50.5	11.0	385	2	US-09-107-532A-5871	Sequence 5871, Ap	837	50	10.8	261	2	US-09-543-681A-5280	Sequence 5280, A
825	50.5	11.0	411	2	US-09-902-540-10575	Sequence 10575, Ap	838	50	10.8	261	2	US-09-328-352-4486	Sequence 4486, Ap
826	50.5	11.0	424	2	US-09-902-540-10575	Sequence 10575, Ap	839	50	10.8	264	2	US-09-188-452A-266	Sequence 266, App
827	50.5	11.0	426	2	US-09-902-540-11296	Sequence 11296, A	840	50	10.8	267	2	US-09-134-000C-6206	Sequence 6206, A
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830	50.5	11.0	455	2	US-09-543-681A-7043	Sequence 7043, Ap	843	50	10.8	279	2	US-09-134-001C-4878	Sequence 4878, Ap
831	50.5	11.0	467	2	US-09-107-532A-5964	Sequence 5964, Ap	844	50	10.8	303	2	US-09-543-681A-5154	Sequence 5154, Ap
832	50.5	11.0	467	2	US-09-902-540-11298	Sequence 11298, A	845	50	10.8	303	1	US-08-164-292B-18	Sequence 18, Appli
833	50.5	11.0	476	2	US-10-142-835-28	Sequence 28, Appli	846	50	10.8	308	1	US-08-845-623-18	Sequence 18, Appli
834	50.5	11.0	477	2	US-09-252-991A-29825	Sequence 29825, A	847	50	10.8	308	2	US-08-815-927-18	Sequence 18, Appli
835	50.5	11.0	499	2	US-09-252-991A-27221	Sequence 27221, A	848	50	10.8	308	2	US-09-103-330-18	Sequence 330, Appli
836	50.5	11.0	529	1	US-07-891-942G-8	Sequence 8, Appli	849	50	10.8	308	2	US-09-435-242-18	Sequence 242, App
837	50.5	11.0	529	1	US-08-370-909-19	Sequence 19, Appli	850	50	10.8	322	2	US-09-252-991A-24657	Sequence 24657, A
838	50.5	11.0	529	1	US-08-504-046-8	Sequence 8, Appli	851	50	10.8	323	2	US-09-107-532A-6263	Sequence 6263, App

852	50	10.8	326	2	US-09-784-810C-11	Sequence 11, Appl	925	49.5	10.7	372	1	US-08-626-665A-8	Sequence 8, Appl
853	50	10.8	356	2	US-09-125-619-2	Sequence 2, Appl	926	49.5	10.7	372	2	US-08-993-088A-2	Sequence 20, Appl
854	50	10.8	356	2	US-09-125-619-13	Sequence 13, Appl	927	49.5	10.7	372	2	US-08-993-088A-20	Sequence 2, Appl
855	50	10.8	356	2	US-10-222-566-2	Sequence 2, Appl	928	49.5	10.7	372	2	US-08-993-424B-2	Sequence 2, Appl
856	50	10.8	356	2	US-10-222-566-13	Sequence 13, Appl	929	49.5	10.7	372	2	US-08-665-034A-2	Sequence 2, Appl
857	50	10.8	356	2	US-10-143-024A-2	Sequence 2, Appl	930	49.5	10.7	372	2	US-08-665-034A-4	Sequence 4, Appl
858	50	10.8	356	2	US-10-143-024A-13	Sequence 13, Appl	931	49.5	10.7	372	2	US-09-595-549-9	Sequence 9, Appl
859	50	10.8	356	2	US-10-222-162-2	Sequence 2, Appl	932	49.5	10.7	372	2	US-09-603-680-2	Sequence 2, Appl
860	50	10.8	356	2	US-10-222-162-13	Sequence 13, Appl	933	49.5	10.7	372	2	US-09-603-680-20	Sequence 20, Appl
861	50	10.8	358	2	US-09-270-767-45037	Sequence 45037, A	934	49.5	10.7	372	2	US-08-981-700A-2	Sequence 2, Appl
862	50	10.8	378	2	US-09-502-540-11860	Sequence 11860, A	935	49.5	10.7	372	2	US-08-899-112B-8	Sequence 8, Appl
863	50	10.8	390	2	US-09-710-279-1422	Sequence 1422, Ap	936	49.5	10.7	372	2	US-09-011-553-2	Sequence 2, Appl
864	50	10.8	427	2	US-09-902-540-15413	Sequence 15413, A	937	49.5	10.7	378	2	US-09-689-486-62	Sequence 62, Appl
865	50	10.8	436	2	US-08-584-760A-67	Sequence 67, Appl	938	49.5	10.7	380	2	US-09-120-359-76	Sequence 76, Appl
866	50	10.8	440	2	US-08-584-760A-1	Sequence 1, Appl	939	49.5	10.7	380	2	US-09-515-039-76	Sequence 76, Appl
867	50	10.8	447	2	US-10-162-012-29	Sequence 29, Appl	940	49.5	10.7	380	2	US-08-860-255A-5	Sequence 5, Appl
868	50	10.8	461	2	US-09-543-681A-6448	Sequence 6448, Ap	941	49.5	10.7	394	2	US-09-710-279-3392	Sequence 3292, Ap
869	50	10.8	468	2	US-09-498-612-6	Sequence 6, Appl	942	49.5	10.7	403	2	US-09-489-039A-11022	Sequence 11022, A
870	50	10.8	471	2	US-09-784-810C-6	Sequence 6, Appl	943	49.5	10.7	414	2	US-09-710-279-806	Sequence 806, Ap
871	50	10.8	501	2	US-09-252-991A-13885	Sequence 31885, A	944	49.5	10.7	420	2	US-09-252-991A-3048	Sequence 3048, A
872	50	10.8	521	2	US-09-134-001C-4290	Sequence 4290, Ap	945	49.5	10.7	423	2	US-09-134-001C-3599	Sequence 3599, Ap
873	50	10.8	525	2	US-09-949-016-7407	Sequence 7407, Ap	946	49.5	10.7	427	2	US-09-328-352-6602	Sequence 6602, Ap
874	50	10.8	533	2	US-09-549-519-31	Sequence 31, Appl	947	49.5	10.7	436	2	US-09-902-540-9717	Sequence 9717, Ap
875	50	10.8	544	2	US-09-252-991A-26096	Sequence 26096, A	948	49.5	10.7	462	2	US-09-886-319A-72	Sequence 72, Appl
876	50	10.8	605	2	US-09-949-016-8269	Sequence 8269, Ap	949	49.5	10.7	469	2	US-08-753-007A-8	Sequence 8, Appl
877	50	10.8	606	2	US-09-538-029-798	Sequence 798, App	950	49.5	10.7	469	2	US-09-398-456-8	Sequence 3775, Ap
878	50	10.8	641	2	US-09-653-274-13	Sequence 13, Appl	951	49.5	10.7	470	2	US-10-104-047-3775	Sequence 3778, Ap
879	50	10.8	641	2	US-10-461-791-13	Sequence 13, Appl	952	49.5	10.7	476	2	US-09-134-001C-3778	Sequence 15018, A
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881	50	10.8	1070	2	US-09-653-274-8	Sequence 8, Appl	954	49.5	10.7	507	2	US-09-780-016-2	Sequence 2, Appl
882	50	10.8	1070	2	US-10-461-791-4	Sequence 4, Appl	955	49.5	10.7	507	2	US-10-214-811-2	Sequence 2, Appl
883	50	10.8	1086	2	US-09-653-274-4	Sequence 4, Appl	956	49.5	10.7	507	2	US-10-766-074-2	Sequence 20, Appl
884	50	10.8	1086	2	US-10-461-791-4	Sequence 4, Appl	957	49.5	10.7	532	2	US-09-780-016-20	Sequence 20, Appl
885	50	10.8	1309	2	US-09-862-027-82	Sequence 82, Appl	958	49.5	10.7	532	2	US-10-214-811-20	Sequence 20, Appl
886	50	10.8	1381	2	US-08-826-134-4	Sequence 4, Appl	959	49.5	10.7	532	2	US-10-766-074-20	Sequence 20, Appl
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888	50	10.8	1479	1	US-08-840-063-2	Sequence 2, Appl	974	49.5	10.7	563	2	US-08-931-608A-3	Sequence 3, Appl
889	49.5	10.7	58	1	US-08-721-746-2	Sequence 2, Appl	975	49.5	10.7	563	2	US-09-851-847-3	Sequence 3, Appl
890	49.5	10.7	58	1	US-09-513-999C-6346	Sequence 6346, Ap	976	49.5	10.7	582	2	US-09-252-991A-11510	Sequence 21510, A
891	49.5	10.7	66	2	US-09-513-999C-7224	Sequence 7224, Ap	977	49.5	10.7	597	2	US-09-252-991A-32657	Sequence 32657, A
892	49.5	10.7	160	2	US-09-732-210-304	Sequence 304, App	978	49.5	10.7	607	2	US-09-252-991A-32643	Sequence 32643, A
893	49.5	10.7	160	2	US-09-107-532A-5111	Sequence 5111, Ap	979	49.5	10.7	637	2	US-09-566-611C-35	Sequence 35, Appl
894	49.5	10.7	172	2	US-08-772-270A-1	Sequence 1, Appl	980	49.5	10.7	647	2	US-08-753-007A-32	Sequence 32, Appl
895	49.5	10.7	172	2	US-09-062-126-2	Sequence 2, Appl	981	49.5	10.7	647	2	US-09-398-496-32	Sequence 32, Appl
896	49.5	10.7	193	2	US-09-475-316A-78	Sequence 78, Appl	988	49.5	10.7	660	2	US-09-948-016-6643	Sequence 6643, Ap
897	49.5	10.7	193	2	US-09-704-640-78	Sequence 78, Appl	993	49.5	10.7	660	2	US-09-689-486-58	Sequence 58, Appl
898	49.5	10.7	200	1	US-08-698-805-6	Sequence 6, Appl	997	49.5	10.7	661	2	US-09-252-991A-7070	Sequence 27070, A
899	49.5	10.7	212	2	US-09-813-453B-59	Sequence 59, Appl	998	49.5	10.7	662	2	US-09-902-540-12594	Sequence 12594, A
900	49.5	10.7	246	2	US-09-134-001C-5292	Sequence 5292, Ap	999	49.5	10.7	683	2	US-09-946-016-7267	Sequence 7267, Ap
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902	49.5	10.7	249	2	US-09-248-796A-19210	Sequence 19210, A	1001	49.5	10.7	770	2	US-09-538-092-1265	Sequence 1265, Ap
903	49.5	10.7	252	1	US-07-885-089B-7	Sequence 7, Appl	1002	49.5	10.7	1121	2	US-08-915-048A-2	Sequence 2, Appl
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905	49.5	10.7	252	2	US-09-919-039-228	Sequence 228, App	1004	49.5	10.6	63	2	US-09-471-276-1429	Sequence 1429, Ap
906	49.5	10.7	262	2	US-09-134-001C-3746	Sequence 3746, Ap	1005	49.5	10.6	70	2	US-09-248-796A-33339	Sequence 23339, A
907	49.5	10.7	262	2	US-09-710-279-1568	Sequence 1568, Ap	1006	49.5	10.6	103	2	US-09-543-681A-7951	Sequence 7951, Ap
908	49.5	10.7	265	2	US-09-780-016-8	Sequence 8, Appl	1007	49.5	10.6	118	2	US-09-056-556-231	Sequence 231, App
909	49.5	10.7	265	2	US-10-214-811-8	Sequence 8, Appl	1008	49.5	10.6	118	2	US-09-072-596-226	Sequence 226, App
910	49.5	10.7	268	2	US-10-766-074-8	Sequence 8, Appl	1009	49.5	10.6	118	2	US-09-072-596-226	Sequence 226, App
911	49.5	10.7	290	2	US-09-716-964B-156	Sequence 156, App	1010	49.5	10.6	118	2	US-10-193-002-226	Sequence 226, App
912	49.5	10.7	290	2	US-09-780-016-6	Sequence 6, Appl	1011	49.5	10.6	118	2	US-10-084-848B-24	Sequence 24, Appl
913	49.5	10.7	290	2	US-10-214-811-6	Sequence 6, Appl	1012	49.5	10.6	156	2	US-09-134-001C-4234	Sequence 4234, Ap
914	49.5	10.7	290	2	US-10-766-074-6	Sequence 6, Appl	1013	49.5	10.6	190	2	US-09-475-316A-29	Sequence 29, Appl
915	49.5	10.7	296	2	US-09-489-847-293	Sequence 293, App	1014	49.5	10.6	190	2	US-09-475-316A-31	Sequence 31, Appl
916	49.5	10.7	315	2	US-09-107-532A-5917	Sequence 5917, Ap	1015	49.5	10.6	190	2	US-09-704-640-29	Sequence 29, Appl
917	49.5	10.7	319	2	US-09-852-991A-28066	Sequence 28066, A	1016	49.5	10.6	190	2	US-09-704-640-31	Sequence 31, Appl
918	49.5	10.7	320	2	US-09-489-039A-10349	Sequence 10349, A	1017	49.5	10.6	195	1	US-08-403-852B-25	Sequence 25, Appl
919	49.5	10.7	322	2	US-09-949-016-11381	Sequence 11381, A	1018	49.5	10.6	195	2	US-08-510-646B-24	Sequence 24, Appl
920	49.5	10.7	324	2	US-09-602-787A-284	Sequence 484, App	1019	49.5	10.6	195	2	US-09-231-818-24	Sequence 24, Appl
921	49.5	10.7	328	2	US-09-605-703B-2840	Sequence 2840, Ap	1020	49.5	10.6	195	2	US-09-489-039A-11088	Sequence 11088, A
922	49.5	10.7	353	2	US-09-489-039A-12270	Sequence 12270, A	1021	49.5	10.6	195	2	US-09-635-359B-24	Sequence 24, Appl
923	49.5	10.7	363	2	US-09-949-016-11040	Sequence 11040, A	1022	49.5	10.6	210	2	US-09-270-767-57495	Sequence 57495, A
924	49.5	10.7	364	2	US-09-489-039A-10066	Sequence 10066, A	1023	49.5	10.6	219	2	US-09-461-325-151	Sequence 151, App

1034	49	10.6	219	2	US-10-012-542-151	Sequence 151, App	1097	49	10.6	629	4	PCT-US92-09382-8	Sequence 8, Appl
1035	49	10.6	219	2	US-10-115-121-151	Sequence 151, App	1098	49	10.6	644	2	US-09-949-016-9507	Sequence 9507, App
1026	49	10.6	228	2	US-09-543-681A-6856	Sequence 6856, App	1099	49	10.6	649	2	US-09-248-796A-20641	Sequence 20641, App
1027	49	10.6	230	2	US-09-134-000C-5011	Sequence 5011, App	1100	49	10.6	659	2	US-09-238-986-75	Sequence 75, Appl
1028	49	10.6	231	2	US-09-893-737-154	Sequence 154, App	1101	49	10.6	659	2	US-10-101-464A-75	Sequence 75, Appl
1029	49	10.6	235	2	US-09-902-540-15987	Sequence 15987, App	1102	49	10.6	677	2	US-09-252-991A-32924	Sequence 32924, App
1030	49	10.6	239	2	US-08-913-014A-3	Sequence 3, Appl	1103	49	10.6	681	2	US-09-270-767-42219	Sequence 42219, App
1031	49	10.6	239	2	US-09-653-285-3	Sequence 3, Appl	1104	49	10.6	719	2	US-08-765-907A-15	Sequence 15, Appl
1032	49	10.6	249	2	US-09-813-453B-70	Sequence 70, Appl	1105	49	10.6	719	2	US-09-987-614A-15	Sequence 15, Appl
1033	49	10.6	259	2	US-09-543-681A-7362	Sequence 7362, App	1106	49	10.6	722	2	US-09-617-145-2	Sequence 2, Appl
1034	49	10.6	262	2	US-09-069-821-4	Sequence 4, Appl	1107	49	10.6	722	2	US-09-949-016-6418	Sequence 6418, App
1035	49	10.6	262	2	US-09-956-086-4	Sequence 4, Appl	1108	49	10.6	726	2	US-09-248-796A-17362	Sequence 17362, App
1036	49	10.6	262	2	US-09-956-087-4	Sequence 4, Appl	1109	49	10.6	740	2	US-09-022-983-5	Sequence 5, Appl
1037	49	10.6	263	2	US-09-489-039A-12047	Sequence 12047, A	1110	49	10.6	742	2	US-09-949-016-11569	Sequence 11569, App
1038	49	10.6	266	2	US-09-134-000C-3847	Sequence 3847, App	1111	49	10.6	785	2	US-09-079-030-216	Sequence 216, App
1039	49	10.6	274	2	US-09-489-039A-13041	Sequence 13041, A	1112	49	10.6	787	2	US-09-489-039A-7628	Sequence 7628, App
1040	49	10.6	282	2	US-09-420-592A-7	Sequence 7, Appl	1113	49	10.6	839	2	US-09-538-092-274	Sequence 274, App
1041	49	10.6	282	2	US-09-985-443-7	Sequence 7, Appl	1114	49	10.6	862	2	US-09-328-352-5527	Sequence 5527, App
1042	49	10.6	282	2	US-09-983-580-7	Sequence 7, Appl	1115	49	10.6	908	2	US-09-635-872A-15	Sequence 15, Appl
1043	49	10.6	291	2	US-09-902-540-15435	Sequence 15435, A	1116	49	10.6	908	2	US-09-636-077A-15	Sequence 15, Appl
1044	49	10.6	327	2	US-09-949-016-7336	Sequence 7336, App	1117	49	10.6	908	2	US-09-636-060C-15	Sequence 15, Appl
1045	49	10.6	331	2	US-08-765-963-1	Sequence 1, Appl	1118	49	10.6	908	2	US-09-986-552-15	Sequence 15, Appl
1046	49	10.6	332	2	US-09-328-352-4745	Sequence 4745, App	1119	49	10.6	908	2	US-09-636-596C-15	Sequence 15, Appl
1047	49	10.6	342	2	US-08-785-928-1	Sequence 1, Appl	1120	49	10.6	908	2	US-10-023-894-9	Sequence 9, Appl
1048	49	10.6	342	2	US-08-728-603-17	Sequence 17, Appl	1121	49	10.6	908	2	US-10-306-886-15	Sequence 15, Appl
1049	49	10.6	345	2	US-09-328-352-4841	Sequence 4841, App	1122	49	10.6	908	2	US-09-895-072-15	Sequence 15, Appl
1050	49	10.6	349	2	US-08-630-172-6	Sequence 6, Appl	1123	49	10.6	908	2	US-10-023-888-9	Sequence 9, Appl
1051	49	10.6	349	2	US-09-375-419-6	Sequence 6, Appl	1124	49	10.6	914	2	US-09-193-562D-28	Sequence 28, Appl
1052	49	10.6	349	2	US-09-134-001C-4004	Sequence 4004, App	1125	49	10.6	914	2	US-09-623-624-6	Sequence 6, Appl
1053	49	10.6	352	2	US-08-466-343D-2	Sequence 2, Appl	1126	49	10.6	914	2	US-10-055-412B-28	Sequence 28, Appl
1054	49	10.6	352	2	US-09-087-232A-13	Sequence 13, Appl	1127	49	10.6	914	2	US-10-270-595-6	Sequence 6, Appl
1055	49	10.6	352	2	US-08-861-105-14	Sequence 14, Appl	1128	49	10.6	946	2	US-09-902-540-16817	Sequence 16817, A
1056	49	10.6	352	2	US-08-575-967A-2	Sequence 2, Appl	1129	49	10.6	984	2	US-09-409-604-4	Sequence 4, Appl
1057	49	10.6	352	2	US-09-045-583-52	Sequence 52, Appl	1130	49	10.6	1070	1	US-08-633-770A-2	Sequence 2, Appl
1058	49	10.6	352	2	US-09-517-605-5	Sequence 5, Appl	1131	49	10.6	1070	2	US-09-280-197-6	Sequence 6, Appl
1059	49	10.6	352	2	US-09-534-185-52	Sequence 52, Appl	1132	49	10.6	1070	2	US-09-423-126-4	Sequence 4, Appl
1060	49	10.6	352	2	US-08-833-752-5	Sequence 5, Appl	1133	49	10.6	1073	2	US-09-180-245-2	Sequence 2, Appl
1061	49	10.6	352	2	US-09-502-783A-2	Sequence 2, Appl	1134	49	10.6	1073	2	US-09-819-249-2	Sequence 2, Appl
1062	49	10.6	352	2	US-09-796-202-1	Sequence 1, Appl	1135	49	10.6	1089	2	US-09-866-510-4	Sequence 4, Appl
1063	49	10.6	352	2	US-09-938-719-5	Sequence 5, Appl	1136	49	10.6	1956	2	US-10-152-886-23	Sequence 23, App
1064	49	10.6	352	2	US-09-502-784A-2	Sequence 2, Appl	1137	48.5	10.5	51	2	US-09-962-756-1637	Sequence 1637, App
1065	49	10.6	352	2	US-09-339-912A-2	Sequence 2, Appl	1138	48.5	10.5	51	2	US-10-067-422-18	Sequence 18, Appl
1066	49	10.6	352	2	US-08-771-276-2	Sequence 2, Appl	1139	48.5	10.5	51	2	US-08-358-160-103	Sequence 103, App
1067	49	10.6	352	2	US-08-771-276-20	Sequence 20, Appl	1140	48.5	10.5	77	2	US-08-311-731A-385	Sequence 385, App
1068	49	10.6	352	2	US-09-939-226B-5	Sequence 5, Appl	1141	48.5	10.5	94	2	US-09-252-991A-29771	Sequence 29771, A
1069	49	10.6	352	2	US-09-195-662A-2	Sequence 2, Appl	1142	48.5	10.5	112	1	US-08-284-393B-4	Sequence 4, Appl
1070	49	10.6	352	2	US-09-949-002-303	Sequence 303, App	1143	48.5	10.5	112	1	US-08-284-393B-14	Sequence 14, Appl
1071	49	10.6	352	2	US-10-323-314-1	Sequence 1, Appl	1144	48.5	10.5	112	2	PCT-US95-08950-4	Sequence 4, Appl
1072	49	10.6	352	2	US-09-938-703B-5	Sequence 5, Appl	1145	48.5	10.5	114	2	US-09-054-711C-4	Sequence 4, Appl
1073	49	10.6	357	2	US-09-949-016-9074	Sequence 9074, App	1146	48.5	10.5	114	2	US-09-054-711C-5	Sequence 5, Appl
1074	49	10.6	358	2	US-09-543-681A-6765	Sequence 4765, App	1147	48.5	10.5	114	2	US-09-679-710B-1	Sequence 1, Appl
1075	49	10.6	367	4	US-08-132-990A-2	Sequence 2, Appl	1148	48.5	10.5	114	2	US-09-679-710B-3	Sequence 3, Appl
1076	49	10.6	367	4	PCT-US92-09382-2	Sequence 2, Appl	1149	48.5	10.5	114	2	US-09-679-710B-2	Sequence 2, Appl
1077	49	10.6	378	2	US-09-949-002-552	Sequence 552, App	1150	48.5	10.5	114	2	US-09-679-710B-4	Sequence 4, Appl
1078	49	10.6	405	2	US-09-252-991A-19717	Sequence 19717, A	1151	48.5	10.5	114	2	US-09-679-710B-5	Sequence 5, Appl
1079	49	10.6	428	2	US-09-248-796A-20582	Sequence 20582, A	1152	48.5	10.5	114	2	US-09-679-710B-6	Sequence 6, Appl
1080	49	10.6	436	2	US-09-134-000C-4843	Sequence 4843, App	1153	48.5	10.5	114	2	US-09-679-710B-7	Sequence 7, Appl
1081	49	10.6	454	2	US-09-270-767-45646	Sequence 45646, A	1154	48.5	10.5	114	2	US-09-679-710B-8	Sequence 8, Appl
1082	49	10.6	463	1	US-08-677-049-6	Sequence 6, Appl	1155	48.5	10.5	114	2	US-09-679-710B-9	Sequence 9, Appl
1083	49	10.6	464	2	US-09-252-991A-26212	Sequence 26212, A	1156	48.5	10.5	114	2	US-09-679-710B-10	Sequence 10, Appl
1084	49	10.6	466	2	US-09-543-681A-8174	Sequence 8174, App	1157	48.5	10.5	114	2	US-09-679-710B-11	Sequence 11, Appl
1085	49	10.6	493	2	US-09-543-681A-6754	Sequence 6754, App	1158	48.5	10.5	114	2	US-09-679-710B-13	Sequence 13, Appl
1086	49	10.6	498	2	US-09-107-532A-7077	Sequence 7077, App	1159	48.5	10.5	114	2	US-09-679-710B-14	Sequence 14, Appl
1087	49	10.6	500	2	US-10-104-047-3456	Sequence 3456, App	1160	48.5	10.5	114	2	US-09-679-710B-15	Sequence 15, Appl
1088	49	10.6	501	2	US-09-252-991A-32473	Sequence 32473, A	1161	48.5	10.5	114	2	US-09-679-710B-16	Sequence 16, Appl
1089	49	10.6	513	2	US-09-488-039A-12877	Sequence 12877, A	1162	48.5	10.5	114	2	US-09-679-710B-17	Sequence 17, Appl
1090	49	10.6	513	2	US-09-488-039A-9932	Sequence 9932, App	1163	48.5	10.5	114	2	US-09-679-710B-18	Sequence 18, Appl
1091	49	10.6	520	2	US-09-540-236-1988	Sequence 1988, App	1164	48.5	10.5	114	2	US-09-679-710B-20	Sequence 20, Appl
1092	49	10.6	526	2	US-09-328-352-8024	Sequence 8024, App	1165	48.5	10.5	114	2	US-09-679-710B-21	Sequence 21, Appl
1093	49	10.6	548	2	US-09-543-681A-6631	Sequence 6631, App	1166	48.5	10.5	114	2	US-09-679-710B-22	Sequence 22, Appl
1094	49	10.6	569	2	US-09-252-991A-25628	Sequence 25628, A	1167	48.5	10.5	114	2	US-09-679-710B-23	Sequence 23, Appl
1095	49	10.6	573	2	US-09-042-709A-19	Sequence 19, Appl	1168	48.5	10.5	114	2	US-09-679-710B-23	Sequence 23, Appl
1096	49	10.6	629	1	US-08-132-990A-8	Sequence 8, Appl	1169	48.5	10.5	114	2	US-09-938-936-1	Sequence 1, Appl

1170	48.5	10.5	114	2	US-09-938-936-3	Sequence 3, Appl1	1243	48.5	10.5	503	2	US-09-605-703B-268	Sequence 268, App
1171	48.5	10.5	114	2	US-09-938-936-4	Sequence 4, Appl1	1244	48.5	10.5	511	2	US-09-679-666B-12	Sequence 12, Appl1
1172	48.5	10.5	114	2	US-09-938-936-5	Sequence 5, Appl1	1245	48.5	10.5	515	2	US-09-438-185A-1021	Sequence 1021, Ap
1173	48.5	10.5	114	2	US-10-053-406-1	Sequence 1, Appl1	1246	48.5	10.5	524	2	US-09-902-540-16272	Sequence 16272, A
1174	48.5	10.5	114	2	US-10-053-406-2	Sequence 2, Appl1	1247	48.5	10.5	540	2	US-09-248-796A-18127	Sequence 18127, A
1175	48.5	10.5	114	2	US-10-053-406-3	Sequence 3, Appl1	1248	48.5	10.5	559	1	US-08-428-125-1	Sequence 1, Appl1
1176	48.5	10.5	114	2	US-10-053-406-4	Sequence 4, Appl1	1249	48.5	10.5	559	1	US-08-426-125-1	Sequence 1, Appl1
1177	48.5	10.5	114	2	US-10-053-406-5	Sequence 5, Appl1	1250	48.5	10.5	599	1	US-08-455-355-3	Sequence 3, Appl1
1178	48.5	10.5	114	2	US-10-053-406-6	Sequence 6, Appl1	1251	48.5	10.5	599	1	US-08-455-355-3	Sequence 3, Appl1
1179	48.5	10.5	114	2	US-10-053-406-7	Sequence 7, Appl1	1252	48.5	10.5	599	2	US-09-367-512-1	Sequence 1, Appl1
1180	48.5	10.5	114	2	US-10-053-406-8	Sequence 8, Appl1	1253	48.5	10.5	599	2	US-10-407-339-1	Sequence 1, Appl1
1181	48.5	10.5	114	2	US-10-053-406-9	Sequence 9, Appl1	1254	48.5	10.5	608	2	US-09-769-787-8	Sequence 8, Appl1
1182	48.5	10.5	114	2	US-10-053-406-10	Sequence 10, Appl1	1255	48.5	10.5	638	1	US-08-426-125-4	Sequence 4, Appl1
1183	48.5	10.5	114	2	US-10-053-406-11	Sequence 11, Appl1	1256	48.5	10.5	638	1	US-08-455-355-4	Sequence 4, Appl1
1184	48.5	10.5	114	2	US-10-053-406-13	Sequence 13, Appl1	1257	48.5	10.5	638	2	US-09-367-512-3	Sequence 3, Appl1
1185	48.5	10.5	114	2	US-10-053-406-14	Sequence 14, Appl1	1258	48.5	10.5	638	2	US-10-407-339-3	Sequence 3, Appl1
1186	48.5	10.5	114	2	US-10-053-406-15	Sequence 15, Appl1	1259	48.5	10.5	655	2	US-09-134-001C-5531	Sequence 5531, Ap
1187	48.5	10.5	114	2	US-10-053-406-16	Sequence 16, Appl1	1260	48.5	10.5	684	2	US-09-252-991A-24618	Sequence 24618, A
1188	48.5	10.5	114	2	US-10-053-406-17	Sequence 17, Appl1	1261	48.5	10.5	787	2	US-09-252-991A-28939	Sequence 28939, A
1189	48.5	10.5	114	2	US-10-053-406-18	Sequence 18, Appl1	1262	48.5	10.5	815	2	US-09-489-039A-12469	Sequence 12469, A
1190	48.5	10.5	114	2	US-10-053-406-19	Sequence 19, Appl1	1263	48.5	10.5	825	2	US-09-489-039A-8469	Sequence 8469, Ap
1191	48.5	10.5	114	2	US-10-053-406-20	Sequence 20, Appl1	1264	48.5	10.5	938	2	US-09-637-145-2	Sequence 2, Appl1
1192	48.5	10.5	114	2	US-10-053-406-21	Sequence 21, Appl1	1265	48.5	10.5	1052	2	US-09-949-016-1508	Sequence 11508, A
1193	48.5	10.5	114	2	US-10-053-406-22	Sequence 22, Appl1	1266	48.5	10.5	1161	2	US-09-327-536-2	Sequence 6043, Ap
1194	48.5	10.5	114	2	US-10-053-406-23	Sequence 23, Appl1	1267	48.5	10.5	1278	2	US-09-134-000C-6043	Sequence 12469, A
1195	48.5	10.5	132	2	US-08-012-543-2	Sequence 2, Appl1	1268	48.5	10.5	1501	1	US-08-447-464-3	Sequence 3, Appl1
1196	48.5	10.5	132	2	US-09-054-711C-3	Sequence 3, Appl1	1269	48.5	10.5	1501	1	US-08-716-679-3	Sequence 3, Appl1
1197	48.5	10.5	132	2	US-09-462-941-19	Sequence 19, Appl1	1270	48.5	10.5	1884	2	US-09-538-009-1329	Sequence 1329, Ap
1198	48.5	10.5	132	2	US-09-949-016-6187	Sequence 6187, Ap	1271	48.5	10.5	4545	1	US-08-804-227C-14	Sequence 14, Appl1
1199	48.5	10.5	132	4	PCT-US93-07645A-2	Sequence 2, Appl1	1272	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1200	48.5	10.5	132	4	PCT-US93-07645-2	Sequence 2, Appl1	1273	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1201	48.5	10.5	136	2	US-09-378-238-33	Sequence 33, Appl1	1274	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1202	48.5	10.5	136	2	US-09-626-896-29	Sequence 29, Appl1	1275	48.5	10.5	28	2	US-09-952-756-1457	Sequence 1457, Ap
1203	48.5	10.5	136	2	US-09-841-730-29	Sequence 29, Appl1	1276	48.5	10.5	70	2	US-09-252-991A-16917	Sequence 16917, A
1204	48.5	10.5	137	2	US-09-270-767-31676	Sequence 31676, A	1277	48.5	10.5	73	2	US-09-489-847-300	Sequence 300, App
1205	48.5	10.5	137	2	US-09-270-767-46893	Sequence 46893, A	1278	48.5	10.5	74	2	US-09-489-847-229	Sequence 229, App
1206	48.5	10.5	150	2	US-09-949-016-7926	Sequence 7926, Ap	1279	48.5	10.5	76	2	US-09-962-756-2182	Sequence 2182, Ap
1207	48.5	10.5	157	2	US-09-378-238-31	Sequence 31, Appl1	1280	48.5	10.5	86	2	US-10-002-344A-186	Sequence 186, App
1208	48.5	10.5	157	2	US-09-626-896-27	Sequence 27, Appl1	1281	48.5	10.5	120	2	US-09-931-381A-12	Sequence 12, Appl1
1209	48.5	10.5	157	2	US-09-841-730-27	Sequence 27, Appl1	1282	48.5	10.5	120	2	US-09-513-999C-4290	Sequence 4290, Ap
1210	48.5	10.5	198	2	US-09-489-039A-7760	Sequence 7760, Ap	1283	48.5	10.5	120	2	US-09-898-753A-14	Sequence 14, Appl1
1211	48.5	10.5	217	2	US-09-352-991A-30489	Sequence 30489, A	1284	48.5	10.5	133	2	US-09-071-033C-226	Sequence 226, App
1212	48.5	10.5	217	2	US-09-248-796A-19579	Sequence 19579, A	1285	48.5	10.5	133	2	US-09-489-039A-8313	Sequence 8313, Ap
1213	48.5	10.5	249	1	US-07-885-089B-2	Sequence 2, Appl1	1286	48.5	10.5	136	2	US-09-270-767-40016	Sequence 40016, A
1214	48.5	10.5	256	1	US-07-885-089B-8	Sequence 8, Appl1	1287	48.5	10.5	136	2	US-09-270-767-31783	Sequence 31783, A
1215	48.5	10.5	256	2	US-09-198-452A-449	Sequence 449, App	1288	48.5	10.5	136	2	US-09-270-767-47000	Sequence 47000, A
1216	48.5	10.5	256	2	US-09-543-681A-4282	Sequence 4282, Ap	1289	48.5	10.5	142	2	US-09-621-976-4460	Sequence 4460, Ap
1217	48.5	10.5	257	2	US-09-438-185A-432	Sequence 432, App	1290	48.5	10.5	143	2	US-09-857-612A-2	Sequence 2, Appl1
1218	48.5	10.5	258	1	US-08-665-202-5	Sequence 5, Appl1	1291	48.5	10.5	145	2	US-09-134-000C-6051	Sequence 6051, Ap
1219	48.5	10.5	258	2	US-09-315-574-51	Sequence 51, Appl1	1292	48.5	10.5	153	2	US-09-621-976-5179	Sequence 5179, Ap
1220	48.5	10.5	279	2	US-09-328-352-4717	Sequence 4717, Ap	1293	48.5	10.5	160	2	US-09-248-796A-31952	Sequence 31952, A
1221	48.5	10.5	285	2	US-08-992-035A-1	Sequence 1, Appl1	1294	48.5	10.5	166	2	US-09-328-352-4665	Sequence 4665, Ap
1222	48.5	10.5	285	2	US-09-952-991A-32954	Sequence 32954, A	1295	48.5	10.5	170	2	US-09-489-039A-8313	Sequence 8313, Ap
1223	48.5	10.5	293	2	US-09-660-587A-40	Sequence 40, Appl1	1296	48.5	10.5	180	2	US-09-270-767-40016	Sequence 40016, A
1224	48.5	10.5	293	2	US-09-314-701-44	Sequence 44, Appl1	1297	48.5	10.5	187	2	US-09-270-767-35232	Sequence 55232, A
1225	48.5	10.5	293	2	US-09-811-007A-40	Sequence 40, Appl1	1298	48.5	10.5	187	2	US-09-270-767-33761	Sequence 33761, A
1226	48.5	10.5	293	2	US-10-314-639-44	Sequence 44, Appl1	1299	48.5	10.5	192	2	US-09-475-316A-35	Sequence 25, Appl1
1227	48.5	10.5	293	2	US-10-059-964A-44	Sequence 44, Appl1	1300	48.5	10.5	192	2	US-09-475-316A-87	Sequence 87, Appl1
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ALIGNMENTS

Sequence 10643, A
Sequence 14, Appl
Sequence 6, Appl
Sequence 5, Appl
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Sequence 3058, Ap
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Sequence 269, Appl
Sequence 10, Appl
Sequence 58, Appl
Sequence 5740, Ap
Sequence 54, Appl
Sequence 38876, A
Sequence 54093, A
Sequence 52, Appl

RESULT 1
US-09-289-349-11
Sequence 11, Application US/09289349
Patent No. 6277574
GENERAL INFORMATION:
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APPLICANT: Azimzai, Yalda
APPLICANT: Yue, Henry
TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
FILE REFERENCE: PB-0010 US
CURRENT APPLICATION NUMBER: US/09/289,349
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: 1900433CD1
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Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MERVTLALLLGLTLEANDPFPANKDPPFYDMKNLQSLICGGLTAIAGIAVLSGK 60
Qy 61 CKYKSKQKSPVPEKAIPLITPGSATTC 89
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RESULT 2
Sequence 262, Application US/09991181
Patent No. 6913919
GENERAL INFORMATION:
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APPLICANT: Baker, Kevin P.
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APPLICANT: Gurney, Auelin L.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tanabe, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087607
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PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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Query Match 100.0%; Score 461; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred.No. 2e-51;
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RESULT 3
 ; Sequence 262; Application US/09990444
 ; Patent No. 6930170
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Auecin L.
APPLICANT: Kijavln, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/390,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boctstein, David
; APPLICANT: Debnoyers, Luc
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; APPLICANT: Baton, Dan L.
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; APPLICANT: Watanabe, Colin K.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 100.0%; Score 461; DB 2; Length 89;
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RESULT 5
Sequence 262, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Ivar J.
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/087609
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472

Qy 60 KCKYSSQKOSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 8

US-08-738-127-5
Sequence 5, Application US/08738127
Patent No. 5919655
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Philip R.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738.127
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0141 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 951423
US-08-738-127-5

Query Match 55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.2e-25;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

Qy 1 MERTVLA-LLLAGTALTEANDPPYDKKNTQLSGLLTAGIAAVLSG 59
Db 1 MEGITCALVLAGLPLEVLEANGP-VDKSPFYDWESLQSGMTFGLLCTAGIAMALSG 59
Qy 60 KCKYSSQKOSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 9

US-09-213-392-5
Sequence 5, Application US/09213392
Patent No. 5943505
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213.392
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083,661
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0128 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 951423
US-09-213-392-5

Query Match 55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.2e-25;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

Qy 1 MERTVLA-LLLAGTALTEANDPPYDKKNTQLSGLLTAGIAAVLSG 59
Db 1 MEGITCALVLAGLPLEVLEANGP-VDKSPFYDWESLQSGMTFGLLCTAGIAMALSG 59
Qy 60 KCKYSSQKOSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 10

US-09-083-661-5
Sequence 5, Application US/09083661
Patent No. 5955283
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,661

Qy 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85

RESULT 13
US-08-738-127-4
Sequence 4, Application US/08738127
Patent No. 5919655
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
ADDRESSEE: Hawking, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,127
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0141 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1085026
US-08-738-127-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.9e-20;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

Qy 1 MERVTLALL-LAGLTLEANDPFANKDPPYYDMKNQLSGLTGGLAIAAGIAVLG 59
Db 1 MOKVTLGLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLICAGVLCAMGIITWSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85

RESULT 14
US-09-213-392-4
Sequence 4, Application US/09213392
Patent No. 5945505
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
ADDRESSEE: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,392
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083,661
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0128 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1085026
US-09-213-392-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.9e-20;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

Qy 1 MERVTLALL-LAGLTLEANDPFANKDPPYYDMKNQLSGLTGGLAIAAGIAVLG 59
Db 1 MOKVTLGLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLICAGVLCAMGIITWSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85

RESULT 15
US-09-083-661-4
Sequence 4, Application US/09083661
Patent No. 5955283
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
ADDRESSEE: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 06:28:10 ; Search time 110 Seconds
(without alignments)
338.062 Million cell updates/sec

Perfect score: 461
Sequence: 1 MERYTALLLLAGLTALLEAN.....HSPVEKAIPIITPGSATTTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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626	461	100.0	89	4	US-10-063-742-50
741	461	100.0	89	5	US-10-972-317-50
742	461	100.0	89	5	US-10-820-474A-35
744	461	100.0	89	5	US-10-950-374-262
747	374	81.1	186	4	US-10-295-027-210
748	374	81.1	318	4	US-10-295-027-212
749	276.5	60.0	88	3	US-09-866-050A-698
750	214.5	46.5	87	4	US-10-176-847-24
751	214.5	46.5	87	4	US-10-205-823-140
752	214.5	46.5	87	4	US-10-177-293-168
753	214.5	46.5	87	4	US-10-295-027-1358
754	214.5	46.5	87	6	US-11-051-454-140
755	214.5	46.5	116	4	US-10-161-493-34
756	209.5	45.4	86	4	US-10-161-493-32
762	191.5	41.5	150	3	US-09-925-299-955
763	191.5	41.5	150	3	US-09-981-876-238
764	129	28.0	92	3	US-09-148-545-238
765	129	28.0	92	3	US-09-903-190-120
766	129	28.0	92	3	US-09-978-360A-776
767	129	28.0	92	4	US-10-408-765A-1270
768	129	28.0	92	5	US-10-930-331-120

769	129	28.0	92	5	US-10-979-111-238	Sequence 238, App
770	129	28.0	93	3	US-09-981-876-183	Sequence 183, App
771	129	28.0	93	3	US-09-148-545-183	Sequence 183, App
772	129	28.0	93	5	US-10-979-111-183	Sequence 183, App
773	121	26.2	70	3	US-09-981-876-289	Sequence 289, App
774	121	26.2	70	3	US-09-148-545-269	Sequence 269, App
775	121	26.2	70	5	US-10-979-111-269	Sequence 269, App
776	113.5	24.6	138	4	US-10-291-265-446	Sequence 446, App
777	112.5	24.4	95	4	US-10-291-265-918	Sequence 918, App
778	112.5	24.4	96	3	US-09-809-391-473	Sequence 473, App
779	112.5	24.4	96	3	US-09-882-171-473	Sequence 473, App
780	112.5	24.4	96	4	US-10-164-861-473	Sequence 473, App
807	112.5	24.4	120	3	US-09-997-428-199	Sequence 199, App
1296	112.5	24.4	120	5	US-10-931-886-434	Sequence 434, App
1298	112.5	24.4	120	5	US-10-955-955-434	Sequence 434, App
1299	112.5	24.4	120	5	US-10-950-374-199	Sequence 199, App
1300	106	23.0	69	3	US-09-809-391-606	Sequence 606, App
1301	106	23.0	69	3	US-09-882-171-606	Sequence 606, App
1302	106	23.0	69	4	US-10-164-861-606	Sequence 606, App
1303	105.5	22.9	110	5	US-10-450-763-56705	Sequence 56705, A
1304	94	20.4	115	4	US-10-352-272-2	Sequence 2, Appl1
1305	94	20.4	178	3	US-09-833-245-1532	Sequence 1532, Ap
1306	94	20.4	178	3	US-09-985-153-92	Sequence 92, Appl
1307	94	20.4	178	3	US-09-985-153-93	Sequence 93, Appl
1308	94	20.4	178	3	US-09-985-153-94	Sequence 94, Appl
1309	94	20.4	178	3	US-09-985-153-96	Sequence 96, Appl

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JOB time : 134 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 06:31:05 ; Search time 10 Seconds
(without alignments)
59.933 Million cell updates/sec

Perfect score: 461
Sequence: 1 MERVTLALLAGLTALLEAN.....HSPVEKAIPLITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_AA_New:*
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2: /cgn2_6/pcodata/1/pubppaa/US06_NEW_PUB pep.*
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7: /cgn2_6/pcodata/1/pubppaa/US11_NEW_PUB pep.*
8: /cgn2_6/pcodata/1/pubppaa/US60_NEW_PUB pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	214.5	46.5	87	6	US-10-821-234-1279 Sequence 1279, Ap
3	214.5	46.5	87	7	US-11-080-991-24 Sequence 24, Appl
4	113.5	24.6	138	7	US-11-000-463-446 Sequence 44, Appl
5	112.5	24.4	95	7	US-11-000-463-918 Sequence 918, Appl
7	94	20.4	178	6	US-10-821-234-1495 Sequence 1495, Ap
8	67.5	14.6	664	7	US-11-080-991-40 Sequence 40, Appl
9	61.5	13.3	977	7	US-11-093-274-39 Sequence 93, Appl
10	61	13.2	139	6	US-10-467-657-4932 Sequence 4932, Ap
11	59	12.8	658	6	US-10-613-744-6 Sequence 6, Appl
13	58.5	12.7	837	6	US-10-467-657-1464 Sequence 1464, Ap
14	57.5	12.5	324	6	US-10-858-730-113 Sequence 113, Appl
15	56.5	12.3	148	6	US-10-512-109-19 Sequence 19, Appl
16	55.5	12.0	384	7	US-11-108-185-14 Sequence 14, Appl
17	55.5	12.0	384	7	US-11-108-185-16 Sequence 16, Appl
18	55.5	12.0	384	7	US-11-108-185-18 Sequence 18, Appl
20	54.5	11.8	186	7	US-11-044-899-23 Sequence 23, Appl
21	54.5	11.8	384	7	US-11-108-185-2 Sequence 2, Appl
22	54.5	11.8	384	7	US-11-108-185-4 Sequence 4, Appl
23	54.5	11.8	895	7	US-11-150-406-2 Sequence 2, Appl
24	54.5	11.8	920	6	US-10-821-234-1139 Sequence 1139, Ap
25	54	11.7	346	7	US-11-186-284-189 Sequence 189, Appl
26	54	11.7	376	6	US-10-467-657-6138 Sequence 6138, Ap
27	53.5	11.6	244	7	US-11-186-284-97 Sequence 97, Appl
28	53.5	11.6	407	6	US-10-793-626-1578 Sequence 1578, Ap
30	53.5	11.6	495	6	US-10-613-744-5 Sequence 5, Appl

31	53	11.5	223	7	US-11-055-822-1130 Sequence 1130, Ap
32	53	11.5	267	6	US-10-995-561-552 Sequence 552, Appl
33	53	11.5	267	6	US-10-995-561-553 Sequence 553, Appl
34	52.5	11.4	384	7	US-11-108-185-6 Sequence 6, Appl
35	52.5	11.4	384	7	US-11-108-185-8 Sequence 8, Appl
36	52.5	11.4	384	7	US-11-108-185-10 Sequence 10, Appl
37	52.5	11.4	384	7	US-11-108-185-12 Sequence 12, Appl
38	52	11.3	112	7	US-11-000-463-282 Sequence 282, Appl
39	52	11.3	112	7	US-11-000-463-754 Sequence 754, Appl
40	52	11.3	378	7	US-11-082-389-404 Sequence 404, Appl
41	52	11.3	401	7	US-11-000-365-50 Sequence 50, Appl
42	52	11.3	401	7	US-11-032-794-50 Sequence 50, Appl
43	52	11.3	628	7	US-11-082-389-402 Sequence 402, Appl
44	52	11.3	711	6	US-10-467-657-2966 Sequence 2966, Ap
45	51.5	11.2	59	6	US-10-689-747-174 Sequence 174, Appl
46	51.5	11.2	211	6	US-10-965-972-1 Sequence 1, Appl
47	51.5	11.2	211	6	US-11-186-284-22 Sequence 22, Appl
48	51.5	11.2	244	6	US-10-510-386-110 Sequence 110, Appl
49	51.5	11.2	312	7	US-11-082-389-346 Sequence 346, Appl
50	51	11.1	265	6	US-10-467-657-5894 Sequence 5894, Ap
51	51	11.1	265	6	US-10-467-657-7494 Sequence 7494, Ap
52	51	11.1	280	7	US-11-143-980-34 Sequence 34, Appl
53	51	11.1	421	6	US-10-467-657-790 Sequence 790, Appl
54	51	11.1	774	7	US-11-000-463-439 Sequence 439, Appl
55	50.5	11.0	1211	7	US-11-186-284-4 Sequence 4, Appl
56	50	10.8	82	6	US-10-467-657-4684 Sequence 4684, Ap
57	50	10.8	334	6	US-10-467-657-2204 Sequence 2204, Ap
58	50	10.8	334	6	US-10-467-657-6504 Sequence 6504, Ap
59	50	10.8	346	7	US-11-000-365-52 Sequence 52, Appl
60	50	10.8	346	7	US-11-032-794-52 Sequence 52, Appl
61	50	10.8	390	6	US-10-793-626-1422 Sequence 1422, Ap
62	50	10.8	457	6	US-10-982-548-8 Sequence 8, Appl
63	50	10.8	457	6	US-10-982-548-13 Sequence 13, Appl
64	49.5	10.7	252	6	US-10-821-234-1445 Sequence 1445, Ap
65	49.5	10.7	252	7	US-11-186-284-8 Sequence 8, Appl
66	49.5	10.7	362	6	US-10-793-626-1568 Sequence 1568, Ap
67	49.5	10.7	394	6	US-10-793-626-1392 Sequence 1392, Ap
68	49.5	10.7	414	6	US-10-793-626-806 Sequence 806, Appl
69	49.5	10.7	557	7	US-11-191-375-4 Sequence 4, Appl
70	49.5	10.7	557	7	US-11-191-375-4 Sequence 4, Appl
71	49	10.6	276	6	US-10-467-657-6 Sequence 6, Appl
72	49	10.6	276	6	US-10-467-657-4158 Sequence 4158, Ap
73	49	10.6	349	6	US-10-485-517-417 Sequence 417, Appl
74	49	10.6	352	6	US-10-995-561-523 Sequence 523, Appl
75	49	10.6	352	7	US-11-068-686-2 Sequence 2, Appl
76	49	10.6	352	7	US-11-068-686-20 Sequence 20, Appl
77	49	10.6	417	6	US-10-485-517-419 Sequence 419, Appl
78	49	10.6	468	7	US-11-167-273-1 Sequence 1, Appl
79	49	10.6	529	6	US-10-821-234-1168 Sequence 1168, Ap
80	49	10.6	914	7	US-11-108-172-1066 Sequence 1066, Ap
81	49	10.6	914	7	US-11-148-108-41 Sequence 41, Appl
82	49	10.6	914	7	US-11-051-267-29 Sequence 29, Appl
83	48.5	10.5	136	7	US-11-051-267-29 Sequence 29, Appl
84	48.5	10.5	146	7	US-11-061-821-42 Sequence 42, Appl
85	48.5	10.5	157	7	US-11-051-267-27 Sequence 27, Appl
86	48.5	10.5	284	6	US-10-821-234-1280 Sequence 1280, Ap
87	48.5	10.5	505	6	US-10-467-657-2440 Sequence 2440, Ap
88	48.5	10.5	528	6	US-10-467-657-6354 Sequence 6354, Ap
89	48.5	10.5	533	6	US-10-467-657-4328 Sequence 4328, Ap
90	48.5	10.5	567	6	US-10-467-657-4328 Sequence 4328, Ap
91	48.5	10.5	615	6	US-10-982-545-14 Sequence 14, Appl
92	48.5	10.5	616	6	US-10-982-545-5 Sequence 5, Appl
93	48.5	10.5	68	6	US-10-467-657-4718 Sequence 4718, Ap
94	48	10.4	254	7	US-11-067-322-460 Sequence 460, Appl
95	48	10.4	407	7	US-11-092-140-4 Sequence 4, Appl
96	48	10.4	521	7	US-11-105-268-58 Sequence 58, Appl
97	48	10.4	840	6	US-10-645-441-1 Sequence 1, Appl
98	48	10.4	948	6	US-11-485-517-235 Sequence 235, Appl
99	48	10.4	89	7	US-11-123-896-269 Sequence 269, Appl
100	47.5	10.3	107	7	US-11-074-176-10 Sequence 10, Appl
101	47.5	10.3	485	7	US-10-995-561-632 Sequence 632, Appl
102	47.5	10.3	738	6	US-10-995-561-653 Sequence 653, Appl
103	47.5	10.3	738	6	US-10-995-561-653 Sequence 653, Appl
104	47.5	10.3	896	6	US-10-467-657-7004 Sequence 7004, Ap
105	47.5	10.3	896	6	US-10-467-657-7004 Sequence 7004, Ap

106	47	10.2	194	7	US-11-044-899-26	Sequence 26, Appl	179	46	10.0	252	7	US-11-054-515-1852	Sequence 1852, Ap
107	47	10.2	254	7	US-11-067-323-44	Sequence 44, Appl	180	46	10.0	254	7	US-11-067-323-184	Sequence 184, App
108	47	10.2	254	7	US-11-067-323-178	Sequence 178, App	181	46	10.0	254	7	US-11-067-323-188	Sequence 188, App
109	47	10.2	254	7	US-11-067-323-182	Sequence 182, App	182	46	10.0	254	7	US-11-067-323-210	Sequence 210, App
110	47	10.2	254	7	US-11-067-323-192	Sequence 192, App	183	46	10.0	254	7	US-11-067-323-276	Sequence 276, App
111	47	10.2	254	7	US-11-067-323-196	Sequence 196, App	184	46	10.0	254	7	US-11-067-323-320	Sequence 320, App
112	47	10.2	254	7	US-11-067-323-216	Sequence 216, App	185	46	10.0	254	7	US-11-067-323-332	Sequence 332, App
113	47	10.2	254	7	US-11-067-323-218	Sequence 218, App	186	46	10.0	254	7	US-11-067-323-336	Sequence 336, App
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115	47	10.2	254	7	US-11-067-323-222	Sequence 222, App	188	46	10.0	254	7	US-11-067-323-362	Sequence 362, App
116	47	10.2	254	7	US-11-067-323-228	Sequence 228, App	189	46	10.0	254	7	US-11-067-323-368	Sequence 368, App
117	47	10.2	254	7	US-11-067-323-230	Sequence 230, App	190	46	10.0	254	7	US-11-067-323-568	Sequence 568, App
118	47	10.2	254	7	US-11-067-323-252	Sequence 252, App	191	46	10.0	254	7	US-11-067-323-634	Sequence 634, App
119	47	10.2	254	7	US-11-067-323-272	Sequence 272, App	192	46	10.0	254	7	US-11-067-323-636	Sequence 636, App
120	47	10.2	254	7	US-11-067-323-278	Sequence 278, App	193	46	10.0	254	7	US-11-067-323-638	Sequence 638, App
121	47	10.2	254	7	US-11-067-323-282	Sequence 282, App	194	46	10.0	254	7	US-11-067-323-734	Sequence 734, App
122	47	10.2	254	7	US-11-067-323-286	Sequence 286, App	195	46	10.0	255	6	US-10-846-172A-4	Sequence 4, Appli
123	47	10.2	254	7	US-11-067-323-292	Sequence 292, App	196	46	10.0	261	7	US-11-102-240-118	Sequence 118, App
124	47	10.2	254	7	US-11-067-323-294	Sequence 294, App	197	46	10.0	261	7	US-10-846-172A-6	Sequence 2, Appli
125	47	10.2	254	7	US-11-067-323-296	Sequence 296, App	198	46	10.0	268	6	US-10-467-657-5704	Sequence 5704, Ap
126	47	10.2	254	7	US-11-067-323-304	Sequence 304, App	199	46	10.0	304	6	US-10-846-172A-5	Sequence 5, Appli
127	47	10.2	254	7	US-11-067-323-306	Sequence 306, App	200	46	10.0	322	6	US-10-821-224-1092	Sequence 1092, Ap
128	47	10.2	254	7	US-11-067-323-316	Sequence 316, App	201	46	10.0	330	6	US-10-846-172A-7	Sequence 7, Appli
129	47	10.2	254	7	US-11-067-323-326	Sequence 326, App	202	46	10.0	333	6	US-10-846-172A-6	Sequence 6, Appli
130	47	10.2	254	7	US-11-067-323-328	Sequence 328, App	203	46	10.0	377	6	US-10-821-224-1436	Sequence 1436, Ap
131	47	10.2	254	7	US-11-067-323-330	Sequence 330, App	204	46	10.0	407	6	US-11-051-267-825	Sequence 25, Appl
132	47	10.2	254	7	US-11-067-323-334	Sequence 334, App	205	46	10.0	421	6	US-10-793-626-1818	Sequence 1818, Ap
133	47	10.2	254	7	US-11-067-323-352	Sequence 352, App	206	46	10.0	457	6	US-10-995-561-197	Sequence 797, App
134	47	10.2	254	7	US-11-067-323-354	Sequence 354, App	207	46	10.0	466	7	US-11-110-082-53	Sequence 33, Appl
135	47	10.2	254	7	US-11-067-323-358	Sequence 358, App	208	46	10.0	505	6	US-11-063-343-18	Sequence 38, Appl
136	47	10.2	254	7	US-11-067-323-354	Sequence 364, App	209	46	10.0	534	6	US-10-646-283-8	Sequence 2, Appli
137	47	10.2	254	7	US-11-067-323-370	Sequence 370, App	210	46	10.0	858	6	US-10-645-441-25	Sequence 25, Appli
138	47	10.2	254	7	US-11-067-323-374	Sequence 374, App	211	46	10.0	858	6	US-11-071-581-1	Sequence 1, Appli
139	47	10.2	254	7	US-11-067-323-376	Sequence 376, App	212	46	10.0	1046	6	US-10-392-224A-16	Sequence 16, Appli
140	47	10.2	254	7	US-11-067-323-378	Sequence 378, App	213	46	10.0	1210	7	US-11-108-172-692	Sequence 692, App
141	47	10.2	254	7	US-11-067-323-400	Sequence 400, App	214	46	10.0	1548	7	US-11-108-172-1095	Sequence 1095, Ap
142	47	10.2	254	7	US-11-067-323-406	Sequence 406, App	215	46	10.0	1615	7	US-11-108-528-80	Sequence 80, Appl
143	47	10.2	257	6	US-10-793-628-344	Sequence 344, App	216	46	10.0	3002	6	US-10-821-224-116	Sequence 916, App
144	47	10.2	328	6	US-10-485-517-340	Sequence 340, App	217	45	9.9	119	6	US-10-467-657-4694	Sequence 4694, Ap
145	47	10.2	489	6	US-10-858-730-198	Sequence 198, App	218	45	9.9	138	7	US-11-080-991-12	Sequence 12, Appl
146	47	10.2	489	7	US-11-055-822-1152	Sequence 1152, Ap	219	45	9.9	175	6	US-10-467-657-7504	Sequence 7504, Ap
147	47	10.2	544	6	US-10-467-657-2436	Sequence 2436, Ap	220	45	9.9	202	6	US-10-858-730-86	Sequence 86, Appl
148	47	10.2	752	7	US-11-080-991-52	Sequence 52, Appl	221	45	9.9	254	7	US-11-067-323-450	Sequence 450, App
149	47	10.2	1006	6	US-10-467-657-8400	Sequence 8400, Ap	222	45	9.9	254	7	US-11-067-323-574	Sequence 574, App
150	47	10.2	1068	7	US-11-191-374-45	Sequence 45, Appl	223	45	9.9	269	6	US-10-995-561-535	Sequence 535, App
151	47	10.2	1306	6	US-11-191-375-45	Sequence 45, Appl	224	45	9.9	283	6	US-10-632-150-50	Sequence 50, Appl
152	47	10.2	2107	6	US-10-995-561-905	Sequence 905, Appl	225	45	9.9	283	7	US-11-073-457-50	Sequence 50, Appl
153	47	10.2	2480	6	US-10-995-561-897	Sequence 827, App	226	45	9.9	283	7	US-11-073-457-50	Sequence 50, Appl
154	47	10.2	3116	6	US-10-995-561-825	Sequence 825, App	228	45	9.9	286	7	US-11-179-977-9	Sequence 9, Appli
155	47	10.2	67	6	US-10-995-561-826	Sequence 826, App	229	45	9.9	303	6	US-10-995-561-534	Sequence 534, App
156	46.5	10.1	149	7	US-10-986-501-141	Sequence 141, App	230	45	9.9	323	6	US-10-467-657-556	Sequence 556, App
157	46.5	10.1	188	7	US-11-055-822-400	Sequence 406, App	231	45	9.9	354	6	US-10-467-657-5634	Sequence 67, Appl
158	46.5	10.1	307	7	US-11-064-774A-117	Sequence 117, App	232	45	9.9	408	6	US-10-763-712A-67	Sequence 67, Appl
159	46.5	10.1	328	6	US-11-082-389-4	Sequence 4, Appli	233	45	9.9	456	6	US-10-763-712A-66	Sequence 66, Appl
160	46.5	10.1	330	6	US-10-848-375-1	Sequence 1, Appli	234	45	9.9	502	6	US-10-763-712A-68	Sequence 68, Appl
161	46.5	10.1	330	6	US-11-184-380-12	Sequence 12, Appl	235	45	9.9	622	6	US-10-510-386-736	Sequence 236, App
162	46.5	10.1	342	6	US-10-689-742-218	Sequence 218, App	236	45	9.9	792	7	US-11-108-172-1127	Sequence 1127, Ap
163	46.5	10.1	374	7	US-11-051-267-20	Sequence 20, Appl	237	45	9.9	984	7	US-11-055-822-508	Sequence 508, App
164	46.5	10.1	390	7	US-11-184-380-2	Sequence 2, Appli	238	45	9.9	984	7	US-11-055-822-594	Sequence 594, App
165	46.5	10.1	488	6	US-10-821-234-1000	Sequence 1000, Ap	239	45	9.9	1476	6	US-10-647-956A-4	Sequence 4, Appli
166	46.5	10.1	512	6	US-10-467-657-2284	Sequence 2284, Ap	240	45	9.9	1709	6	US-10-995-561-973	Sequence 973, App
167	46.5	10.1	512	6	US-10-467-657-6592	Sequence 6592, Ap	241	45	9.8	111	6	US-10-821-224-1547	Sequence 1547, Ap
168	46.5	10.1	522	7	US-11-055-822-1100	Sequence 1100, Ap	242	45	9.8	160	7	US-11-010-874-16	Sequence 16, Appl
169	46.5	10.1	550	7	US-11-184-380-14	Sequence 14, Appl	243	45	9.8	215	7	US-11-089-551A-15	Sequence 15, Appl
170	46.5	10.1	574	6	US-10-763-712A-6	Sequence 6, Appli	244	45	9.8	237	7	US-11-089-551A-2	Sequence 2, Appli
171	46.5	10.1	603	6	US-10-467-657-5018	Sequence 5018, Ap	245	45	9.8	246	6	US-10-793-626-842	Sequence 542, App
172	46.5	10.1	610	7	US-11-184-380-3	Sequence 3, Appli	246	45	9.8	246	6	US-10-793-626-814	Sequence 814, App
173	46.5	10.1	758	7	US-11-089-551A-31	Sequence 31, Appl	247	45	9.8	271	7	US-11-089-551A-17	Sequence 17, Appl
174	46.5	10.1	842	6	US-10-645-441-2	Sequence 2, Appli	248	45	9.8	310	7	US-11-025-834A-13	Sequence 13, Appl
175	46.5	10.1	1043	6	US-10-392-234A-34	Sequence 34, Appl	249	45	9.8	316	6	US-10-467-657-4414	Sequence 4414, Ap
176	46	10.0	58	6	US-10-613-744-28	Sequence 28, Appl	250	45	9.8	339	7	US-11-010-874-6	Sequence 6, Appli
177	46	10.0	219	6	US-10-846-172A-1	Sequence 1, Appli	251	45	9.8	434	7	US-11-082-389-556	Sequence 256, Appl
178	46	10.0	250	7	US-11-054-515-1222	Sequence 1222, Ap	252	45	9.8	534	7	US-11-075-185-17	Sequence 17, Appl

253	45	9.8	563	6	US-10-878-556A-135	Sequence 135, App	329	44	9.5	254	7	US-11-067-323-226	Sequence 226, App
254	45	9.8	646	6	US-10-793-626-676	Sequence 676, App	330	44	9.5	254	7	US-11-067-323-234	Sequence 234, App
255	45	9.8	649	7	US-11-102-240-132	Sequence 132, App	331	44	9.5	254	7	US-11-067-323-236	Sequence 236, App
256	45	9.8	685	7	US-11-089-551A-2	Sequence 2, Appl	332	44	9.5	254	7	US-11-067-323-238	Sequence 238, App
257	45	9.8	753	7	US-11-186-284-153	Sequence 153, App	333	44	9.5	254	7	US-11-067-323-240	Sequence 240, App
258	45	9.8	858	6	US-10-878-556A-36	Sequence 36, Appl	334	44	9.5	254	7	US-11-067-323-242	Sequence 242, App
259	45	9.8	903	7	US-11-057-058-65	Sequence 65, Appl	335	44	9.5	254	7	US-11-067-323-244	Sequence 244, App
260	45	9.8	1069	7	US-11-191-374-17	Sequence 17, Appl	336	44	9.5	254	7	US-11-067-323-246	Sequence 246, App
261	45	9.8	1069	7	US-11-191-375-17	Sequence 17, Appl	337	44	9.5	254	7	US-11-067-323-248	Sequence 248, App
262	45	9.8	1451	6	US-10-995-561-829	Sequence 829, App	338	44	9.5	254	7	US-11-067-323-250	Sequence 250, App
263	45	9.8	1458	6	US-11-096-274-2	Sequence 2, Appl	339	44	9.5	254	7	US-11-067-323-258	Sequence 258, App
264	45	9.7	98	6	US-10-467-657-6904	Sequence 6904, Ap	340	44	9.5	254	7	US-11-067-323-260	Sequence 260, App
265	44.5	9.7	124	6	US-10-467-657-6904	Sequence 6904, Ap	341	44	9.5	254	7	US-11-067-323-262	Sequence 262, App
266	44.5	9.7	145	6	US-10-512-109-21	Sequence 21, Appl	342	44	9.5	254	7	US-11-067-323-264	Sequence 264, App
267	44.5	9.7	168	6	US-10-467-657-6012	Sequence 6012, Ap	343	44	9.5	254	7	US-11-067-323-266	Sequence 266, App
268	44.5	9.7	186	7	US-11-044-899-21	Sequence 21, Appl	344	44	9.5	254	7	US-11-067-323-268	Sequence 268, App
269	44.5	9.7	186	7	US-11-044-899-22	Sequence 22, Appl	345	44	9.5	254	7	US-11-067-323-270	Sequence 270, App
270	44.5	9.7	190	6	US-10-467-657-2540	Sequence 2540, Ap	346	44	9.5	254	7	US-11-067-323-274	Sequence 274, App
271	44.5	9.7	198	7	US-11-082-389-302	Sequence 302, App	347	44	9.5	254	7	US-11-067-323-280	Sequence 280, App
272	44.5	9.7	244	6	US-10-793-626-566	Sequence 566, App	348	44	9.5	254	7	US-11-067-323-284	Sequence 284, App
273	44.5	9.7	255	6	US-10-510-386-66	Sequence 66, Appl	349	44	9.5	254	7	US-11-067-323-288	Sequence 288, App
274	44.5	9.7	255	6	US-10-386-156	Sequence 156, App	350	44	9.5	254	7	US-11-067-323-300	Sequence 300, App
275	44.5	9.7	281	7	US-11-082-389-304	Sequence 304, App	351	44	9.5	254	7	US-11-067-323-302	Sequence 302, App
276	44.5	9.7	304	6	US-10-467-657-7616	Sequence 7616, Ap	352	44	9.5	254	7	US-11-067-323-308	Sequence 308, App
278	44.5	9.7	310	7	US-11-025-834A-15	Sequence 15, Appl	353	44	9.5	254	7	US-11-067-323-310	Sequence 310, App
279	44.5	9.7	321	6	US-10-821-234-1192	Sequence 1192, Ap	354	44	9.5	254	7	US-11-067-323-312	Sequence 312, App
280	44.5	9.7	345	6	US-10-467-657-7598	Sequence 7598, Ap	355	44	9.5	254	7	US-11-067-323-314	Sequence 314, App
281	44.5	9.7	362	6	US-10-821-234-1148	Sequence 1148, Ap	356	44	9.5	254	7	US-11-067-323-318	Sequence 318, App
282	44.5	9.7	418	6	US-10-995-561-753	Sequence 753, App	357	44	9.5	254	7	US-11-067-323-324	Sequence 324, App
283	44.5	9.7	418	6	US-10-995-561-754	Sequence 754, App	358	44	9.5	254	7	US-11-067-323-334	Sequence 334, App
284	44.5	9.7	418	6	US-10-995-561-755	Sequence 755, App	359	44	9.5	254	7	US-11-067-323-338	Sequence 338, App
285	44.5	9.7	418	6	US-10-995-561-756	Sequence 756, App	360	44	9.5	254	7	US-11-067-323-348	Sequence 348, App
286	44.5	9.7	418	6	US-10-995-561-757	Sequence 757, App	361	44	9.5	254	7	US-11-067-323-350	Sequence 350, App
287	44.5	9.7	418	6	US-10-995-561-758	Sequence 758, App	362	44	9.5	254	7	US-11-067-323-356	Sequence 356, App
288	44.5	9.7	418	6	US-10-995-561-759	Sequence 759, App	363	44	9.5	254	7	US-11-067-323-360	Sequence 360, App
289	44.5	9.7	433	7	US-11-055-822-154	Sequence 154, App	364	44	9.5	254	7	US-11-067-323-366	Sequence 366, App
290	44.5	9.7	449	7	US-11-071-062-1	Sequence 1, Appl	365	44	9.5	254	7	US-11-067-323-368	Sequence 368, App
291	44.5	9.7	449	7	US-11-196-459-2	Sequence 2, Appl	366	44	9.5	254	7	US-11-067-323-384	Sequence 384, App
292	44.5	9.7	475	7	US-11-074-176-336	Sequence 336, App	367	44	9.5	254	7	US-11-067-323-388	Sequence 388, App
293	44.5	9.7	488	7	US-11-074-176-126	Sequence 126, App	368	44	9.5	254	7	US-11-067-323-392	Sequence 392, App
294	44.5	9.7	514	6	US-10-821-234-1511	Sequence 1511, Ap	369	44	9.5	254	7	US-11-067-323-394	Sequence 394, App
295	44.5	9.7	525	6	US-10-467-657-5462	Sequence 5462, Ap	370	44	9.5	254	7	US-11-067-323-396	Sequence 396, App
296	44.5	9.7	530	6	US-10-467-657-3804	Sequence 3804, Ap	371	44	9.5	254	7	US-11-067-323-398	Sequence 398, App
297	44.5	9.7	727	6	US-10-793-626-2862	Sequence 2862, Ap	372	44	9.5	254	7	US-11-067-323-402	Sequence 402, App
299	44.5	9.7	909	7	US-11-186-284-2	Sequence 2, Appl	373	44	9.5	254	7	US-11-067-323-404	Sequence 404, App
300	44.5	9.7	913	6	US-10-821-234-1040	Sequence 1040, Ap	374	44	9.5	254	7	US-11-067-323-408	Sequence 408, App
301	44.5	9.7	918	6	US-10-995-561-696	Sequence 696, App	375	44	9.5	254	7	US-11-067-323-410	Sequence 410, App
302	44.5	9.7	1065	7	US-11-191-374-16	Sequence 16, Appl	376	44	9.5	254	7	US-11-067-323-412	Sequence 412, App
303	44.5	9.7	1065	7	US-11-191-375-16	Sequence 16, Appl	377	44	9.5	254	7	US-11-067-323-414	Sequence 414, App
304	44.5	9.7	1167	6	US-10-601-368-18	Sequence 18, Appl	378	44	9.5	254	7	US-11-067-323-418	Sequence 418, App
305	44.5	9.7	1167	6	US-11-192-967-6	Sequence 6, Appl	379	44	9.5	254	7	US-11-067-323-420	Sequence 420, App
306	44.5	9.7	1734	7	US-11-193-715-6	Sequence 6, Appl	380	44	9.5	254	7	US-11-067-323-426	Sequence 426, App
307	44.5	9.7	1734	7	US-10-647-956A-11	Sequence 11, Appl	381	44	9.5	254	7	US-11-067-323-436	Sequence 436, App
308	44.5	9.7	2516	6	US-10-967-527A-2	Sequence 2, Appl	382	44	9.5	254	7	US-11-067-323-444	Sequence 444, App
309	44	9.5	129	6	US-10-821-234-1343	Sequence 1343, Ap	383	44	9.5	254	7	US-11-067-323-542	Sequence 542, App
310	44	9.5	162	6	US-10-880-388-68	Sequence 68, Appl	384	44	9.5	254	7	US-11-067-323-552	Sequence 552, App
311	44	9.5	204	6	US-10-858-730-85	Sequence 85, Appl	385	44	9.5	254	7	US-11-067-323-554	Sequence 554, App
312	44	9.5	229	6	US-11-067-323-98	Sequence 98, Appl	386	44	9.5	254	7	US-11-067-323-584	Sequence 584, App
313	44	9.5	254	7	US-11-067-323-100	Sequence 100, App	387	44	9.5	254	7	US-11-067-323-602	Sequence 602, App
314	44	9.5	254	7	US-11-067-323-156	Sequence 156, App	388	44	9.5	254	7	US-11-067-323-630	Sequence 630, App
315	44	9.5	254	7	US-11-067-323-160	Sequence 160, App	389	44	9.5	254	7	US-11-067-323-732	Sequence 732, App
316	44	9.5	254	7	US-11-067-323-170	Sequence 170, App	390	44	9.5	262	6	US-10-467-657-7532	Sequence 7532, Ap
317	44	9.5	254	7	US-11-067-323-172	Sequence 172, App	391	44	9.5	274	6	US-10-467-657-1326	Sequence 3126, Ap
318	44	9.5	254	7	US-11-067-323-174	Sequence 174, App	392	44	9.5	307	6	US-10-467-657-6016	Sequence 6016, Ap
319	44	9.5	254	7	US-11-067-323-180	Sequence 180, App	393	44	9.5	325	6	US-10-467-657-14	Sequence 14, Appl
320	44	9.5	254	7	US-11-067-323-190	Sequence 190, App	394	44	9.5	325	6	US-10-467-657-5568	Sequence 5568, App
321	44	9.5	254	7	US-11-067-323-194	Sequence 194, App	395	44	9.5	333	6	US-10-949-727A-32	Sequence 326, App
322	44	9.5	254	7	US-11-067-323-198	Sequence 198, App	396	44	9.5	335	6	US-10-957-569-35	Sequence 35, Appl
323	44	9.5	254	7	US-11-067-323-200	Sequence 200, App	397	44	9.5	392	6	US-11-099-691-10	Sequence 10, Appl
324	44	9.5	254	7	US-11-067-323-202	Sequence 202, App	398	44	9.5	519	6	US-10-821-234-864	Sequence 864, App
325	44	9.5	254	7	US-11-067-323-204	Sequence 204, App	399	44	9.5	569	6	US-10-763-712A-34	Sequence 34, Appl
326	44	9.5	254	7	US-11-067-323-208	Sequence 208, App	400	44	9.5	578	6	US-10-858-730-292	Sequence 292, App
327	44	9.5	254	7	US-11-067-323-214	Sequence 214, App	401	44	9.5	610	6		

402	44	9.5	856	6	US-10-467-657-8534	Sequence 8534, App	475	43	9.3	254	7	US-11-067-323-256	Sequence 256, App
403	44	9.5	1730	7	US-11-192-967-4	Sequence 4, App11	476	43	9.3	254	7	US-11-067-323-290	Sequence 290, App
404	44	9.5	1730	7	US-11-193-715-4	Sequence 4, App11	477	43	9.3	254	7	US-11-067-323-322	Sequence 322, App
405	44	9.5	3689	7	US-11-075-185-4	Sequence 4, App11	478	43	9.3	254	7	US-11-067-323-340	Sequence 340, App
406	43.5	9.4	77	6	US-10-467-657-3770	Sequence 3770, App	479	43	9.3	254	7	US-11-067-323-346	Sequence 346, App
407	43.5	9.4	112	7	US-11-082-884-1	Sequence 1, App11	480	43	9.3	254	7	US-11-067-323-372	Sequence 372, App
408	43.5	9.4	132	6	US-10-469-561-22	Sequence 22, App1	481	43	9.3	254	7	US-11-067-323-382	Sequence 382, App
409	43.5	9.4	141	6	US-10-467-657-4110	Sequence 4110, App	482	43	9.3	254	7	US-11-067-323-386	Sequence 386, App
410	43.5	9.4	158	7	US-11-147-047-30	Sequence 30, App1	483	43	9.3	254	7	US-11-067-323-390	Sequence 390, App
411	43.5	9.4	149	7	US-11-147-047-29	Sequence 29, App1	484	43	9.3	254	7	US-11-067-323-468	Sequence 468, App
412	43.5	9.4	183	6	US-10-821-234-1485	Sequence 1485, App	485	43	9.3	254	7	US-11-067-323-478	Sequence 478, App
413	43.5	9.4	183	7	US-11-186-284-111	Sequence 111, App	486	43	9.3	254	7	US-11-067-323-610	Sequence 610, App
414	43.5	9.4	183	7	US-11-186-284-113	Sequence 113, App	487	43	9.3	254	7	US-11-067-323-618	Sequence 618, App
415	43.5	9.4	184	6	US-10-742-634-5	Sequence 5, App11	488	43	9.3	254	7	US-11-067-323-726	Sequence 726, App
416	43.5	9.4	184	6	US-10-967-527A-5	Sequence 5, App11	489	43	9.3	254	7	US-11-067-323-744	Sequence 744, App
417	43.5	9.4	250	7	US-11-054-515-1212	Sequence 1212, App	490	43	9.3	261	6	US-10-467-657-6154	Sequence 6154, App
418	43.5	9.4	254	7	US-11-067-3323-88	Sequence 88, App1	491	43	9.3	280	6	US-10-858-730-200	Sequence 200, App
419	43.5	9.4	254	7	US-11-067-3323-92	Sequence 92, App1	492	43	9.3	422	6	US-10-878-556A-172	Sequence 172, App
420	43.5	9.4	254	7	US-11-067-3323-254	Sequence 254, App	493	43	9.3	443	7	US-11-112-882-29	Sequence 29, App1
421	43.5	9.4	257	7	US-11-054-515-1240	Sequence 1240, App	494	43	9.3	445	7	US-11-194-246-345	Sequence 345, App
422	43.5	9.4	266	6	US-10-884-730-114	Sequence 114, App	495	43	9.3	457	7	US-11-074-176-12	Sequence 12, App1
423	43.5	9.4	266	6	US-11-055-822-620	Sequence 620, App1	496	43	9.3	502	7	US-11-021-441-7	Sequence 7, App11
424	43.5	9.4	276	7	US-11-062-186-40	Sequence 40, App1	497	43	9.3	563	7	US-11-021-441-9	Sequence 9, App11
425	43.5	9.4	292	6	US-10-510-386-74	Sequence 74, App1	498	43	9.3	574	7	US-11-021-441-15	Sequence 15, App1
426	43.5	9.4	309	6	US-10-858-730-364	Sequence 364, App	499	43	9.3	581	7	US-11-021-441-11	Sequence 11, App1
427	43.5	9.4	309	7	US-11-055-822-174	Sequence 174, App	500	43	9.3	581	7	US-10-821-334-1412	Sequence 1412, App
428	43.5	9.4	313	6	US-10-719-311-8	Sequence 8, App11	501	43	9.3	703	6	US-10-821-334-1412	Sequence 1412, App
429	43.5	9.4	334	7	US-11-055-822-980	Sequence 980, App	502	43	9.3	718	6	US-10-467-657-8476	Sequence 8476, App
430	43.5	9.4	338	6	US-10-467-657-3852	Sequence 3852, App	503	43	9.3	737	6	US-10-878-556A-25	Sequence 25, App1
431	43.5	9.4	399	6	US-10-719-311-9	Sequence 9, App11	504	43	9.3	741	7	US-11-089-551A-46	Sequence 46, App1
432	43.5	9.4	407	6	US-10-995-561-1014	Sequence 1014, App	505	43	9.3	856	6	US-10-510-947-8	Sequence 8, App11
433	43.5	9.4	412	6	US-10-793-626-368	Sequence 368, App	506	43	9.3	856	6	US-11-042-988-13	Sequence 13, App1
434	43.5	9.4	412	7	US-11-014-361-2	Sequence 2, App11	507	43	9.3	886	6	US-10-821-334-1390	Sequence 1390, App
435	43.5	9.4	432	7	US-11-140-417-4	Sequence 4, App11	508	43	9.3	1035	7	US-11-021-441-4	Sequence 4, App11
436	43.5	9.4	438	7	US-11-140-417-2	Sequence 2, App11	509	43	9.3	2011	7	US-11-080-991-56	Sequence 56, App1
437	43.5	9.4	451	6	US-10-793-626-2908	Sequence 2908, App	510	43	9.3	3655	7	US-11-075-185-5	Sequence 5, App11
438	43.5	9.4	537	6	US-10-719-311-10	Sequence 10, App1	511	43	9.3	7102	7	US-11-143-980-8	Sequence 8, App11
439	43.5	9.4	592	6	US-10-623-155-169	Sequence 169, App	512	42.5	9.2	117	7	US-11-114-848-2	Sequence 2, App11
440	43.5	9.4	621	7	US-11-184-380-26	Sequence 26, App1	513	42.5	9.2	140	7	US-11-102-240-90	Sequence 90, App1
441	43.5	9.4	623	6	US-10-719-311-2	Sequence 2, App11	514	42.5	9.2	141	6	US-10-982-145-70	Sequence 70, App1
442	43.5	9.4	623	6	US-10-719-311-11	Sequence 11, App1	515	42.5	9.2	141	6	US-10-982-145-71	Sequence 71, App1
443	43.5	9.4	689	7	US-11-113-424-47	Sequence 47, App1	516	42.5	9.2	148	6	US-10-467-657-4330	Sequence 4330, App
444	43.5	9.4	750	6	US-10-689-732-86	Sequence 86, App1	517	42.5	9.2	154	6	US-11-055-822-894	Sequence 894, App
445	43.5	9.4	782	6	US-10-821-234-1592	Sequence 1592, App	518	42.5	9.2	167	6	US-10-821-234-1589	Sequence 1589, App
446	43.5	9.4	791	6	US-10-623-155-170	Sequence 170, App	519	42.5	9.2	225	6	US-10-793-626-1452	Sequence 1452, App
447	43.5	9.4	825	6	US-10-995-561-679	Sequence 679, App	520	42.5	9.2	250	7	US-11-082-389-216	Sequence 216, App
448	43.5	9.4	852	7	US-11-104-923A-5	Sequence 5, App11	521	42.5	9.2	266	7	US-11-102-240-2	Sequence 2, App11
449	43.5	9.4	881	6	US-10-623-155-430	Sequence 430, App	522	42.5	9.2	283	6	US-10-467-657-5210	Sequence 5210, App
450	43.5	9.4	920	6	US-10-623-155-337	Sequence 337, App	523	42.5	9.2	288	6	US-10-793-626-1118	Sequence 1118, App
451	43.5	9.4	932	6	US-10-623-155-161	Sequence 161, App	524	42.5	9.2	329	6	US-10-858-730-108	Sequence 108, App
452	43.5	9.4	1032	6	US-10-392-234A-67	Sequence 67, App1	525	42.5	9.2	342	7	US-11-082-389-214	Sequence 214, App
453	43.5	9.4	1342	6	US-10-770-726-63	Sequence 63, App1	526	42.5	9.2	345	6	US-10-512-109-17	Sequence 17, App1
454	43.5	9.4	1342	7	US-11-113-202-12	Sequence 12, App1	527	42.5	9.2	346	7	US-11-077-386-24	Sequence 24, App1
455	43.5	9.4	1342	7	US-11-113-202-14	Sequence 14, App1	528	42.5	9.2	347	6	US-10-467-657-2962	Sequence 2962, App
456	43.5	9.4	1377	6	US-10-467-657-7822	Sequence 7822, App	529	42.5	9.2	351	6	US-10-821-234-969	Sequence 969, App
457	43.5	9.4	1389	6	US-10-467-657-334	Sequence 334, App	530	42.5	9.2	365	7	US-11-102-978-9	Sequence 9, App11
458	43.5	9.4	5405	6	US-11-108-172-1116	Sequence 1116, App	531	42.5	9.2	365	7	US-11-080-991-78	Sequence 78, App1
459	43.5	9.3	58	6	US-10-613-744-29	Sequence 29, App1	532	42.5	9.2	400	7	US-11-077-386-26	Sequence 26, App1
460	43	9.3	87	7	US-11-053-076-99	Sequence 99, App1	533	42.5	9.2	450	7	US-11-087-100-20	Sequence 20, App1
461	43	9.3	91	7	US-11-123-896-466	Sequence 466, App	534	42.5	9.2	450	7	US-11-087-100-28	Sequence 28, App1
462	43	9.3	179	7	US-11-102-240-154	Sequence 154, App	535	42.5	9.2	450	7	US-11-087-084-20	Sequence 20, App1
463	43	9.3	179	7	US-11-177-987-43	Sequence 43, App1	536	42.5	9.2	450	7	US-11-087-084-28	Sequence 28, App1
464	43	9.3	188	7	US-11-100-183-27	Sequence 27, App1	537	42.5	9.2	450	7	US-11-087-085-20	Sequence 20, App1
465	43	9.3	202	6	US-10-467-657-18	Sequence 18, App1	538	42.5	9.2	450	7	US-11-087-085-28	Sequence 28, App1
466	43	9.3	202	6	US-10-467-657-5702	Sequence 5702, App	539	42.5	9.2	466	6	US-10-878-556A-31	Sequence 31, App1
467	43	9.3	216	6	US-10-485-517-180	Sequence 180, App	540	42.5	9.2	468	6	US-10-467-657-776	Sequence 776, App
468	43	9.3	229	6	US-11-102-240-48	Sequence 48, App1	541	42.5	9.2	534	7	US-11-077-386-25	Sequence 25, App1
469	43	9.3	243	6	US-10-467-657-3362	Sequence 3362, App	542	42.5	9.2	595	6	US-10-995-561-995	Sequence 995, App
470	43	9.3	244	6	US-10-467-657-8278	Sequence 8278, App	543	42.5	9.2	631	6	US-10-995-561-546	Sequence 546, App
471	43	9.3	254	7	US-11-067-323-186	Sequence 186, App	544	42.5	9.2	668	7	US-11-113-424-112	Sequence 112, App1
472	43	9.3	254	7	US-11-067-323-212	Sequence 212, App	546	42.5	9.2	684	6	US-10-793-626-2098	Sequence 2098, App
473	43	9.3	254	7	US-11-067-323-224	Sequence 224, App	547	42.5	9.2	776	6	US-10-925-970-3	Sequence 3, App11
474	43	9.3	254	7	US-11-067-323-232	Sequence 232, App	548	42.5	9.2	824	6	US-10-821-234-1008	Sequence 1008, App

549	42.5	9.2	1073	6	US-10-467-657-5230	Sequence 5230, Ap	623	41.5	9.0	181	6	US-10-467-657-6074	Sequence 6074, Ap
550	42.5	9.2	1124	7	US-11-195-197-9	Sequence 9, Appl	624	41.5	9.0	199	6	US-10-793-626-1342	Sequence 1342, Ap
551	42.5	9.2	1148	7	US-11-110-083-29	Sequence 29, Appl	625	41.5	9.0	196	6	US-10-995-561-992	Sequence 902, Ap
552	42.5	9.2	1149	7	US-11-110-083-30	Sequence 30, Appl	626	41.5	9.0	207	6	US-10-467-657-1944	Sequence 1944, Ap
553	42.5	9.2	1151	7	US-11-046-346-1	Sequence 1, Appl	627	41.5	9.0	216	7	US-11-082-389-32	Sequence 32, Appl
554	42.5	9.2	2059	7	US-11-087-100-4	Sequence 4, Appl	628	41.5	9.0	236	6	US-10-995-561-903	Sequence 903, Appl
555	42.5	9.2	2059	7	US-11-087-084-4	Sequence 4, Appl	629	41.5	9.0	251	6	US-10-793-626-3050	Sequence 3050, Ap
556	42.5	9.2	2059	7	US-11-087-085-4	Sequence 4, Appl	630	41.5	9.0	254	7	US-11-067-323-94	Sequence 96, Appl
557	42.5	9.2	3433	6	US-10-714-781A-67	Sequence 67, Appl	631	41.5	9.0	254	7	US-11-067-323-96	Sequence 96, Appl
558	42	9.1	166	6	US-10-467-657-1722	Sequence 1722, Ap	632	41.5	9.0	254	7	US-11-067-323-150	Sequence 150, Appl
559	42	9.1	166	7	US-11-194-246-418	Sequence 418, Ap	633	41.5	9.0	254	7	US-11-067-323-152	Sequence 152, Appl
560	42	9.1	205	6	US-10-821-234-968	Sequence 968, Appl	634	41.5	9.0	254	7	US-11-067-323-154	Sequence 154, Appl
561	42	9.1	219	6	US-10-793-626-966	Sequence 966, Appl	635	41.5	9.0	254	7	US-11-067-323-158	Sequence 158, Appl
562	42	9.1	237	7	US-11-074-176-178	Sequence 178, Appl	636	41.5	9.0	254	7	US-11-067-323-164	Sequence 164, Appl
563	42	9.1	254	7	US-11-067-323-428	Sequence 428, Appl	637	41.5	9.0	254	7	US-11-067-323-166	Sequence 166, Appl
564	42	9.1	254	7	US-11-067-323-480	Sequence 480, Appl	638	41.5	9.0	254	7	US-11-067-323-168	Sequence 168, Appl
565	42	9.1	254	7	US-11-067-323-482	Sequence 482, Appl	639	41.5	9.0	254	7	US-11-067-323-176	Sequence 176, Appl
566	42	9.1	254	7	US-11-067-323-484	Sequence 484, Appl	640	41.5	9.0	254	7	US-11-067-323-446	Sequence 446, Appl
567	42	9.1	254	7	US-11-067-323-486	Sequence 486, Appl	641	41.5	9.0	254	7	US-11-067-323-652	Sequence 652, Appl
568	42	9.1	254	7	US-11-067-323-488	Sequence 488, Appl	642	41.5	9.0	254	7	US-11-067-323-654	Sequence 654, Appl
569	42	9.1	254	7	US-11-067-323-548	Sequence 548, Appl	643	41.5	9.0	254	6	US-10-821-234-1304	Sequence 1304, Ap
570	42	9.1	254	7	US-11-067-323-558	Sequence 558, Appl	644	41.5	9.0	325	7	US-11-055-822-126	Sequence 126, Appl
571	42	9.1	254	7	US-11-067-323-564	Sequence 564, Appl	646	41.5	9.0	345	7	US-11-073-603-6	Sequence 6, Appl
572	42	9.1	254	7	US-11-067-323-628	Sequence 628, Appl	647	41.5	9.0	345	7	US-11-064-774A-149	Sequence 149, Appl
573	42	9.1	254	7	US-11-067-323-632	Sequence 632, Appl	648	41.5	9.0	353	6	US-10-793-626-634	Sequence 634, Appl
574	42	9.1	254	7	US-11-067-323-718	Sequence 718, Appl	649	41.5	9.0	378	6	US-10-995-561-891	Sequence 891, Appl
575	42	9.1	254	7	US-11-067-323-736	Sequence 736, Appl	650	41.5	9.0	394	6	US-10-793-626-194	Sequence 194, Appl
576	42	9.1	254	7	US-11-067-323-951	Sequence 951, Appl	651	41.5	9.0	394	7	US-11-074-176-310	Sequence 310, Appl
577	42	9.1	254	7	US-11-067-323-987	Sequence 987, Appl	652	41.5	9.0	408	6	US-10-467-657-2048	Sequence 2048, Ap
578	42	9.1	254	7	US-11-067-323-1003	Sequence 1003, Ap	653	41.5	9.0	414	7	US-11-074-176-46	Sequence 46, Appl
579	42	9.1	254	7	US-11-067-323-1079	Sequence 1079, Ap	654	41.5	9.0	419	6	US-10-821-234-1664	Sequence 1664, Ap
580	42	9.1	307	6	US-10-508-263-113	Sequence 113, Appl	655	41.5	9.0	462	7	US-11-105-864-8	Sequence 8, Appl
581	42	9.1	311	7	US-11-055-822-246	Sequence 246, Appl	656	41.5	9.0	468	7	US-11-055-822-68	Sequence 68, Appl
582	42	9.1	341	6	US-10-858-730-124	Sequence 124, Appl	658	41.5	9.0	513	7	US-11-102-240-124	Sequence 124, Appl
583	42	9.1	348	6	US-10-793-626-2866	Sequence 2866, Ap	659	41.5	9.0	528	6	US-10-858-730-88	Sequence 88, Appl
584	42	9.1	348	6	US-10-467-657-8350	Sequence 8350, Ap	660	41.5	9.0	528	6	US-10-467-657-1042	Sequence 1042, Appl
585	42	9.1	349	7	US-11-147-047-47	Sequence 47, Appl	662	41.5	9.0	574	6	US-10-763-712A-1	Sequence 1, Appl
586	42	9.1	351	7	US-11-067-884-4	Sequence 4, Appl	663	41.5	9.0	574	6	US-10-763-712A-102	Sequence 102, Appl
587	42	9.1	351	6	US-10-793-626-2040	Sequence 2040, Ap	664	41.5	9.0	647	7	US-11-080-991-32	Sequence 32, Appl
588	42	9.1	394	6	US-10-821-234-1194	Sequence 1194, Ap	665	41.5	9.0	657	7	US-11-080-991-48	Sequence 48, Appl
589	42	9.1	410	6	US-10-793-626-3258	Sequence 3258, Ap	666	41.5	9.0	657	7	US-11-110-082-37	Sequence 37, Appl
590	42	9.1	428	6	US-10-689-742-50	Sequence 50, Appl	667	41.5	9.0	745	6	US-10-858-730-224	Sequence 224, Appl
591	42	9.1	444	7	US-11-074-176-170	Sequence 170, Appl	668	41.5	9.0	745	7	US-11-055-822-226	Sequence 226, Appl
592	42	9.1	461	7	US-11-132-285-6	Sequence 6, Appl	669	41.5	9.0	745	7	US-11-055-822-714	Sequence 714, Appl
593	42	9.1	463	7	US-11-182-946-4	Sequence 4, Appl	670	41.5	9.0	745	7	US-11-055-822-756	Sequence 756, Appl
594	42	9.1	463	6	US-10-821-234-1094	Sequence 1094, Ap	671	41.5	9.0	745	7	US-11-168-476-2	Sequence 2, Appl
595	42	9.1	477	6	US-10-793-626-3250	Sequence 3250, Ap	672	41.5	9.0	772	7	US-11-147-238-2	Sequence 2, Appl
597	42	9.1	488	6	US-10-467-657-2362	Sequence 2362, Ap	673	41.5	9.0	772	7	US-11-147-238-5	Sequence 5, Appl
598	42	9.1	497	7	US-11-143-980-61	Sequence 61, Appl	674	41.5	9.0	787	6	US-10-467-657-2832	Sequence 2832, Ap
599	42	9.1	548	7	US-11-137-465-47	Sequence 47, Appl	675	41.5	9.0	887	6	US-10-467-657-3960	Sequence 3960, Ap
600	42	9.1	550	6	US-10-467-657-234	Sequence 234, Appl	676	41.5	9.0	904	6	US-10-967-664A-14	Sequence 14, Appl
601	42	9.1	550	6	US-10-467-657-924	Sequence 924, Appl	677	41.5	9.0	1018	7	US-11-067-122-17	Sequence 17, Appl
602	42	9.1	582	6	US-10-793-626-1080	Sequence 1080, Ap	678	41.5	9.0	1259	6	US-10-467-657-5510	Sequence 5510, Ap
603	42	9.1	601	6	US-10-995-561-993	Sequence 993, Appl	679	41.5	9.0	1707	7	US-11-135-885-35	Sequence 35, Appl
604	42	9.1	623	6	US-10-467-657-6260	Sequence 6260, Ap	680	41.5	9.0	1907	7	US-11-039-389-25	Sequence 25, Appl
605	42	9.1	635	6	US-10-995-561-996	Sequence 996, Appl	681	41.5	9.0	67	7	US-11-082-389-324	Sequence 394, Appl
606	42	9.1	686	6	US-10-821-234-1027	Sequence 1027, Ap	682	41	8.9	68	6	US-10-821-234-855	Sequence 855, Appl
607	42	9.1	688	6	US-10-821-234-1533	Sequence 1533, Ap	683	41	8.9	122	6	US-10-821-234-1638	Sequence 1638, Ap
608	42	9.1	716	6	US-10-467-657-6200	Sequence 6200, Ap	684	41	8.9	126	6	US-10-467-657-2240	Sequence 2240, Ap
609	42	9.1	744	6	US-10-467-657-1936	Sequence 1936, Ap	685	41	8.9	139	6	US-10-878-556A-117	Sequence 117, Appl
610	42	9.1	759	6	US-10-467-657-4186	Sequence 4186, Ap	686	41	8.9	154	7	US-11-082-584-14	Sequence 14, Appl
611	42	9.1	774	7	US-11-077-886-34	Sequence 34, Appl	687	41	8.9	161	6	US-10-821-234-1378	Sequence 1278, Ap
612	42	9.1	837	6	US-10-995-561-698	Sequence 998, Appl	688	41	8.9	166	6	US-10-793-626-1576	Sequence 1576, Ap
613	42	9.1	858	6	US-10-878-556A-113	Sequence 113, Appl	689	41	8.9	185	6	US-10-821-234-1498	Sequence 1498, Ap
614	42	9.1	1174	6	US-10-995-561-697	Sequence 997, Appl	690	41	8.9	185	6	US-10-529-118-2	Sequence 2, Appl
615	42	9.1	1356	6	US-10-995-561-904	Sequence 904, Appl	691	41	8.9	193	7	US-11-186-284-157	Sequence 157, Appl
616	42	9.1	1356	7	US-10-995-561-906	Sequence 906, Appl	692	41	8.9	193	7	US-11-186-284-159	Sequence 159, Appl
617	42	9.1	1503	7	US-11-087-100-6	Sequence 6, Appl	693	41	8.9	197	6	US-10-467-657-4944	Sequence 4944, Ap
618	42	9.1	1503	7	US-11-087-084-6	Sequence 6, Appl	694	41	8.9	209	6	US-10-793-626-1698	Sequence 1698, Ap
619	42	9.1	1503	7	US-11-087-085-6	Sequence 6, Appl	695	41	8.9	209	6	US-10-467-657-8494	Sequence 8494, Ap
620	41.5	9.0	74	6	US-10-467-657-4176	Sequence 4176, Ap	696	41	8.9	223	7	US-11-084-716-4	Sequence 4, Appl
621	41.5	9.0	81	6	US-10-821-234-1153	Sequence 1153, Ap	697	41	8.9	238	6	US-10-623-155-1174	Sequence 174, Appl
622	41.5	9.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	698	41	8.9	250	6	US-10-821-234-1542	Sequence 1542, Ap

599	41	8.9	250	7	US-11-054-515-1529	Sequence 1529, Ap	778	40.5	8.8	545	7	US-11-082-389-34	Sequence 34, Appl
700	41	8.9	252	7	US-11-054-515-1994	Sequence 1994, Ap	779	40.5	8.8	585	7	US-11-074-176-190	Sequence 190, Appl
701	41	8.9	252	7	US-11-054-515-2100	Sequence 2100, Ap	780	40.5	8.8	606	6	US-10-624-932-16	Sequence 16, Appl
702	41	8.9	254	7	US-11-054-515-1489	Sequence 1489, Ap	781	40.5	8.8	650	6	US-10-467-657-1948	Sequence 1948, Ap
703	41	8.9	254	7	US-11-067-323-1033	Sequence 1033, Ap	782	40.5	8.8	662	7	US-11-090-439-9	Sequence 9, Appl1
704	41	8.9	254	7	US-11-067-323-1081	Sequence 1081, Ap	783	40.5	8.8	672	6	US-10-467-657-8280	Sequence 8280, Ap
705	41	8.9	264	7	US-11-188-743-24	Sequence 24, Appl	784	40.5	8.8	674	6	US-10-507-275-9	Sequence 9, Appl1
706	41	8.9	264	7	US-11-188-743-25	Sequence 25, Appl	785	40.5	8.8	698	6	US-10-995-561-939	Sequence 939, Appl
707	41	8.9	318	7	US-11-112-882-32	Sequence 32, Appl	787	40.5	8.8	725	6	US-10-995-561-938	Sequence 938, App
708	41	8.9	337	6	US-10-467-962B-97	Sequence 97, Appl	788	40.5	8.8	773	6	US-10-995-561-852	Sequence 852, Appl
709	41	8.9	347	6	US-10-793-626-324	Sequence 324, App	789	40.5	8.8	817	6	US-10-793-626-50	Sequence 50, Appl
710	41	8.9	380	6	US-10-467-657-7258	Sequence 7258, Ap	790	40.5	8.8	817	6	US-10-793-626-1558	Sequence 1528, Ap
711	41	8.9	385	6	US-10-392-234A-22	Sequence 22, Appl	791	40.5	8.8	835	7	US-11-186-283-2	Sequence 2, Appl1
713	41	8.9	405	6	US-10-793-626-2752	Sequence 2752, Ap	792	40.5	8.8	858	6	US-10-995-561-854	Sequence 854, Appl
714	41	8.9	417	6	US-10-793-626-196	Sequence 196, App	793	40.5	8.8	892	6	US-10-507-275-3	Sequence 3, Appl1
715	41	8.9	417	6	US-10-793-626-950	Sequence 950, App	794	40.5	8.8	904	6	US-10-507-275-5	Sequence 5, Appl1
716	41	8.9	425	6	US-10-793-626-1012	Sequence 1012, Ap	795	40.5	8.8	904	7	US-11-087-227-12	Sequence 12, Appl
717	41	8.9	425	6	US-10-793-626-2434	Sequence 2434, Ap	796	40.5	8.8	919	7	US-11-102-240-70	Sequence 70, Appl
718	41	8.9	429	7	US-11-074-176-448	Sequence 248, App	797	40.5	8.8	1162	6	US-10-451-375-3	Sequence 3, Appl1
720	41	8.9	433	6	US-10-467-657-3294	Sequence 3294, Ap	798	40.5	8.8	1178	6	US-10-995-561-851	Sequence 851, Appl
721	41	8.9	443	6	US-10-467-657-7738	Sequence 7738, Ap	799	40.5	8.8	1210	7	US-11-191-374-10	Sequence 10, Appl
722	41	8.9	467	7	US-11-090-439-33	Sequence 33, Appl	800	40.5	8.8	1210	7	US-11-191-375-10	Sequence 10, Appl
723	41	8.9	476	6	US-10-878-556A-158	Sequence 158, App	801	40.5	8.8	1554	7	US-11-186-284-93	Sequence 93, Appl
725	41	8.9	522	7	US-11-080-991-104	Sequence 104, App	802	40.5	8.8	1841	7	US-11-057-058-63	Sequence 63, Appl
726	41	8.9	600	6	US-10-606-302-3	Sequence 3, Appl1	803	40.5	8.8	2261	6	US-10-995-561-600	Sequence 600, App
727	41	8.9	635	6	US-10-821-234-1673	Sequence 1673, Ap	804	40.5	8.8	4384	6	US-10-821-234-1120	Sequence 1120, Ap
729	41	8.9	720	7	US-11-113-424-28	Sequence 28, Appl	805	40	8.7	22	6	US-10-939-890-454	Sequence 454, App
730	41	8.9	747	6	US-11-113-424-26	Sequence 26, Appl	806	40	8.7	100	6	US-10-467-657-6202	Sequence 602, Ap
731	41	8.9	795	6	US-10-821-234-1675	Sequence 1675, Ap	807	40	8.7	108	7	US-11-082-389-278	Sequence 278, App
732	41	8.9	795	6	US-10-770-726-49	Sequence 49, Appl	808	40	8.7	117	7	US-11-000-463-295	Sequence 295, App
733	41	8.9	838	6	US-10-645-441-9	Sequence 9, Appl1	809	40	8.7	117	7	US-11-000-463-767	Sequence 767, App
734	41	8.9	1034	6	US-10-392-234A-30	Sequence 30, Appl	810	40	8.7	159	6	US-10-793-626-878	Sequence 878, App
736	41	8.9	1058	6	US-10-821-234-1473	Sequence 1473, Ap	811	40	8.7	159	6	US-10-793-626-8280	Sequence 2880, Ap
737	41	8.9	1058	6	US-10-878-556A-63	Sequence 63, Appl	812	40	8.7	171	6	US-10-467-657-8576	Sequence 8576, Ap
738	41	8.9	1058	7	US-11-069-642-105	Sequence 105, App	813	40	8.7	195	6	US-10-995-561-563	Sequence 563, App
739	41	8.9	1070	7	US-11/062	Sequence 4, Appl1	814	40	8.7	196	6	US-10-485-517-420	Sequence 420, App
740	41	8.9	1095	7	US-11/062	Sequence 7, Appl1	815	40	8.7	199	6	US-10-967-527A-4	Sequence 4, Appl1
741	41	8.9	1167	6	US-10-942-072-13	Sequence 13, Appl	816	40	8.7	207	6	US-10-467-657-2592	Sequence 2592, Ap
742	41	8.9	1168	6	US-10-942-072-11	Sequence 11, Appl	818	40	8.7	209	6	US-10-467-657-4090	Sequence 4090, Ap
743	41	8.9	118	7	US-11-000-463-274	Sequence 274, Appl	819	40	8.7	220	6	US-10-467-657-64	Sequence 64, Appl
744	40.5	8.8	118	7	US-11-000-463-374	Sequence 746, App	820	40	8.7	228	6	US-10-980-388-17	Sequence 17, Appl
745	40.5	8.8	118	7	US-11-000-463-746	Sequence 746, App	821	40	8.7	232	6	US-10-821-234-1199	Sequence 1199, Appl
746	40.5	8.8	135	6	US-10-793-626-2990	Sequence 2990, Ap	822	40	8.7	237	6	US-10-467-657-4794	Sequence 4794, App
747	40.5	8.8	182	6	US-10-467-657-5380	Sequence 5380, Ap	823	40	8.7	238	6	US-10-467-657-3602	Sequence 3602, Ap
748	40.5	8.8	209	6	US-10-467-657-4336	Sequence 4336, Ap	824	40	8.7	240	6	US-10-467-657-7868	Sequence 7868, Ap
749	40.5	8.8	219	7	US-11-055-822-1082	Sequence 1082, Ap	825	40	8.7	246	6	US-10-467-657-3824	Sequence 3824, Ap
750	40.5	8.8	223	6	US-10-467-657-6830	Sequence 6830, Ap	826	40	8.7	247	7	US-11-000-463-399	Sequence 399, App
751	40.5	8.8	223	6	US-10-467-657-1576	Sequence 1576, Ap	827	40	8.7	252	7	US-11-054-515-1575	Sequence 1575, App
752	40.5	8.8	225	7	US-11-170-653-24	Sequence 24, Appl	828	40	8.7	254	7	US-11-067-323-62	Sequence 62, Appl
753	40.5	8.8	246	6	US-10-467-657-2246	Sequence 2246, Ap	829	40	8.7	254	7	US-11-067-323-64	Sequence 64, Appl
754	40.5	8.8	251	7	US-11-054-515-1837	Sequence 1837, Ap	830	40	8.7	254	7	US-11-067-323-66	Sequence 66, Appl
755	40.5	8.8	252	6	US-10-995-561-601	Sequence 601, App	831	40	8.7	254	7	US-11-067-323-206	Sequence 206, App
756	40.5	8.8	254	7	US-11-067-323-162	Sequence 162, App	832	40	8.7	254	7	US-11-067-323-506	Sequence 506, App
757	40.5	8.8	254	7	US-11-067-323-538	Sequence 538, App	833	40	8.7	254	7	US-11-067-323-536	Sequence 536, App
758	40.5	8.8	257	6	US-10-467-657-176	Sequence 176, App	834	40	8.7	254	7	US-11-067-323-560	Sequence 560, App
759	40.5	8.8	257	6	US-10-467-657-3598	Sequence 3598, Ap	835	40	8.7	254	7	US-11-067-323-586	Sequence 586, App
760	40.5	8.8	301	6	US-10-467-657-7356	Sequence 7356, Ap	836	40	8.7	254	7	US-11-067-323-676	Sequence 676, App
761	40.5	8.8	302	6	US-10-793-626-1144	Sequence 1144, Ap	837	40	8.7	254	7	US-11-067-323-678	Sequence 678, App
762	40.5	8.8	310	6	US-10-485-517-409	Sequence 409, App	838	40	8.7	256	7	US-11-137-465-34	Sequence 34, Appl
764	40.5	8.8	317	7	US-11-129-143-67	Sequence 67, Appl	839	40	8.7	258	7	US-11-000-463-871	Sequence 871, App
765	40.5	8.8	338	7	US-11-074-176-42	Sequence 42, Appl	840	40	8.7	264	7	US-11-055-822-550	Sequence 550, App
766	40.5	8.8	363	6	US-10-995-561-602	Sequence 602, App	841	40	8.7	264	7	US-11-055-822-596	Sequence 596, App
767	40.5	8.8	393	6	US-10-467-657-1038	Sequence 1038, App	843	40	8.7	280	6	US-10-689-742-160	Sequence 160, App
768	40.5	8.8	408	7	US-11-140-417-6	Sequence 6, Appl1	844	40	8.7	292	7	US-11-069-642-117	Sequence 117, App
769	40.5	8.8	423	7	US-11-184-156-2	Sequence 2, Appl1	846	40	8.7	322	6	US-10-508-263-52	Sequence 52, Appl
770	40.5	8.8	478	6	US-10-689-742-184	Sequence 184, App	847	40	8.7	326	6	US-10-793-626-3238	Sequence 3238, App
771	40.5	8.8	482	6	US-10-633-150-14	Sequence 14, Appl	848	40	8.7	333	7	US-11-082-389-202	Sequence 202, App
772	40.5	8.8	482	7	US-11-073-457-14	Sequence 14, Appl	849	40	8.7	337	6	US-10-467-657-4674	Sequence 4674, App
773	40.5	8.8	504	7	US-11-073-460-14	Sequence 14, Appl	850	40	8.7	338	7	US-11-055-822-584	Sequence 584, App
774	40.5	8.8	504	6	US-10-878-556A-126	Sequence 126, App	851	40	8.7	359	7	US-11-012-762-12	Sequence 12, Appl
775	40.5	8.8	512	6	US-10-467-657-2772	Sequence 2772, App	852	40	8.7	370	6	US-10-821-234-1021	Sequence 1021, App
776	40.5	8.8	525	7	US-11-082-389-36	Sequence 36, Appl	853	40	8.7	370	6	US-10-821-234-1105	Sequence 1105, App
777	40.5	8.8	542	7	US-11-153-747-6	Sequence 6, Appl1	854	40	8.7	394	6	US-10-467-657-7966	Sequence 7966, App

855	40	8.7	408	6	US-10-793-626-2286	Sequence 2286, Ap	930	39.5	8.6	254	7	US-11-067-323-12	Sequence 12, Appl
856	40	8.7	409	6	US-10-793-626-2002	Sequence 2002, Ap	931	39.5	8.6	254	7	US-11-067-323-14	Sequence 14, Appl
857	40	8.7	409	6	US-10-793-626-2306	Sequence 2306, Ap	932	39.5	8.6	254	7	US-11-067-323-15	Sequence 16, Appl
858	40	8.7	422	7	US-11-080-248-4	Sequence 4, Appl1	933	39.5	8.6	254	7	US-11-067-323-20	Sequence 20, Appl
859	40	8.7	422	6	US-10-485-517-405	Sequence 405, App	934	39.5	8.6	254	7	US-11-067-323-22	Sequence 22, Appl
860	40	8.7	455	6	US-10-847-867-28	Sequence 28, Appl	935	39.5	8.6	254	7	US-11-067-323-24	Sequence 24, Appl
861	40	8.7	455	6	US-10-847-867-30	Sequence 30, Appl	936	39.5	8.6	254	7	US-11-067-323-26	Sequence 26, Appl
862	40	8.7	455	6	US-10-847-867-31	Sequence 31, Appl	937	39.5	8.6	254	7	US-11-067-323-30	Sequence 30, Appl
863	40	8.7	455	6	US-10-847-867-32	Sequence 32, Appl	938	39.5	8.6	254	7	US-11-067-323-32	Sequence 32, Appl
864	40	8.7	455	6	US-10-847-867-33	Sequence 33, Appl	939	39.5	8.6	254	7	US-11-067-323-34	Sequence 34, Appl
865	40	8.7	455	6	US-10-847-867-34	Sequence 34, Appl	940	39.5	8.6	254	7	US-11-067-323-36	Sequence 36, Appl
866	40	8.7	466	6	US-10-467-657-2360	Sequence 2360, Ap	941	39.5	8.6	254	7	US-11-067-323-40	Sequence 40, Appl
867	40	8.7	479	6	US-10-821-234-871	Sequence 871, App	942	39.5	8.6	254	7	US-11-067-323-42	Sequence 42, Appl
868	40	8.7	494	6	US-10-467-657-4376	Sequence 4376, Ap	943	39.5	8.6	254	7	US-11-067-323-46	Sequence 46, Appl
869	40	8.7	500	6	US-10-821-234-1458	Sequence 1458, Ap	944	39.5	8.6	254	7	US-11-067-323-48	Sequence 48, Appl
871	40	8.7	541	7	US-11-000-463-238	Sequence 238, App	945	39.5	8.6	254	7	US-11-067-323-50	Sequence 50, Appl
872	40	8.7	592	6	US-10-467-657-350	Sequence 550, App	946	39.5	8.6	254	7	US-11-067-323-52	Sequence 52, Appl
873	40	8.7	604	6	US-10-942-072-4	Sequence 4, Appl1	947	39.5	8.6	254	7	US-11-067-323-54	Sequence 54, Appl
874	40	8.7	667	6	US-10-821-234-1477	Sequence 1477, Ap	948	39.5	8.6	254	7	US-11-067-323-56	Sequence 56, Appl
875	40	8.7	692	7	US-11-045-802-26	Sequence 26, Appl	949	39.5	8.6	254	7	US-11-067-323-58	Sequence 58, Appl
876	40	8.7	730	7	US-10-878-556A-99	Sequence 358, App	950	39.5	8.6	254	7	US-11-067-323-60	Sequence 60, Appl
877	40	8.7	737	6	US-10-878-556A-99	Sequence 99, Appl	951	39.5	8.6	254	7	US-11-067-323-68	Sequence 68, Appl
878	40	8.7	757	7	US-11-110-082-35	Sequence 35, Appl	952	39.5	8.6	254	7	US-11-067-323-70	Sequence 70, Appl
879	40	8.7	761	7	US-11-110-082-34	Sequence 34, Appl	953	39.5	8.6	254	7	US-11-067-323-72	Sequence 72, Appl
880	40	8.7	802	6	US-10-510-386-2	Sequence 2, Appl1	954	39.5	8.6	254	7	US-11-067-323-74	Sequence 74, Appl
881	40	8.7	805	6	US-10-485-517-198	Sequence 198, App	955	39.5	8.6	254	7	US-11-067-323-76	Sequence 76, Appl
882	40	8.7	829	6	US-10-512-109-27	Sequence 27, Appl	956	39.5	8.6	254	7	US-11-067-323-78	Sequence 78, Appl
883	40	8.7	874	7	US-11-012-762-8	Sequence 8, Appl1	957	39.5	8.6	254	7	US-11-067-323-80	Sequence 80, Appl
884	40	8.7	882	7	US-11-012-762-34	Sequence 34, Appl	958	39.5	8.6	254	7	US-11-067-323-82	Sequence 82, Appl
886	40	8.7	1015	6	US-10-467-657-180	Sequence 180, App	959	39.5	8.6	254	7	US-11-067-323-84	Sequence 84, Appl
887	40	8.7	1015	6	US-10-467-657-3764	Sequence 3764, Ap	960	39.5	8.6	254	7	US-11-067-323-86	Sequence 86, Appl
888	40	8.7	1029	6	US-10-821-234-908	Sequence 908, App	961	39.5	8.6	254	7	US-11-067-323-90	Sequence 90, Appl
889	40	8.7	1121	7	US-11-113-751-24	Sequence 24, Appl	962	39.5	8.6	254	7	US-11-067-323-102	Sequence 102, App
890	40	8.7	1159	7	US-11-113-751-27	Sequence 27, Appl	963	39.5	8.6	254	7	US-11-067-323-114	Sequence 114, App
891	40	8.7	1167	6	US-10-942-072-6	Sequence 6, Appl1	964	39.5	8.6	254	7	US-11-067-323-112	Sequence 112, App
892	40	8.7	1236	7	US-11-080-991-68	Sequence 68, Appl	965	39.5	8.6	254	7	US-11-067-323-118	Sequence 118, App
893	40	8.7	1363	6	US-10-995-561-1027	Sequence 1027, Ap	966	39.5	8.6	254	7	US-11-067-323-118	Sequence 118, App
894	40	8.7	1463	6	US-10-971-982-3	Sequence 3, Appl1	967	39.5	8.6	254	7	US-11-067-323-120	Sequence 120, App
895	40	8.7	1717	7	US-11-192-967-2	Sequence 2, Appl1	968	39.5	8.6	254	7	US-11-067-323-122	Sequence 122, App
896	40	8.7	1717	7	US-11-193-715-2	Sequence 2, Appl1	969	39.5	8.6	254	7	US-11-067-323-124	Sequence 124, App
897	40	8.7	2047	7	US-11-013-759-4	Sequence 4, Appl1	970	39.5	8.6	254	7	US-11-067-323-126	Sequence 126, App
898	40	8.7	2047	7	US-11-013-759-7	Sequence 7, Appl1	971	39.5	8.6	254	7	US-11-067-323-128	Sequence 128, App
899	40	8.7	3623	6	US-10-995-561-593	Sequence 593, App	972	39.5	8.6	254	7	US-11-067-323-130	Sequence 130, App
900	39.5	8.6	72	7	US-11-053-076-316	Sequence 316, App	973	39.5	8.6	254	7	US-11-067-323-132	Sequence 132, App
901	39.5	8.6	82	6	US-10-467-657-5456	Sequence 5456, Ap	974	39.5	8.6	254	7	US-11-067-323-134	Sequence 134, App
902	39.5	8.6	89	6	US-10-999-866-27	Sequence 27, Appl	975	39.5	8.6	254	7	US-11-067-323-136	Sequence 136, App
903	39.5	8.6	89	7	US-11-061-821-27	Sequence 27, Appl	976	39.5	8.6	254	7	US-11-067-323-138	Sequence 138, App
904	39.5	8.6	91	7	US-11-074-176-352	Sequence 352, App	977	39.5	8.6	254	7	US-11-067-323-140	Sequence 140, App
905	39.5	8.6	95	7	US-11-074-176-180	Sequence 180, App	978	39.5	8.6	254	7	US-11-067-323-142	Sequence 142, App
906	39.5	8.6	111	6	US-10-793-626-730	Sequence 730, App	979	39.5	8.6	254	7	US-11-067-323-144	Sequence 144, App
907	39.5	8.6	113	6	US-10-467-657-1872	Sequence 1872, Ap	980	39.5	8.6	254	7	US-11-067-323-146	Sequence 146, App
908	39.5	8.6	139	6	US-10-793-626-2992	Sequence 2992, Ap	981	39.5	8.6	254	7	US-11-067-323-148	Sequence 148, App
909	39.5	8.6	157	6	US-10-793-626-3268	Sequence 3268, Ap	982	39.5	8.6	254	7	US-11-067-323-228	Sequence 228, App
910	39.5	8.6	173	6	US-10-467-657-772	Sequence 772, App	983	39.5	8.6	254	7	US-11-067-323-422	Sequence 422, App
911	39.5	8.6	211	6	US-10-858-730-102	Sequence 102, App	984	39.5	8.6	254	7	US-11-067-323-426	Sequence 426, App
912	39.5	8.6	214	6	US-10-467-657-5302	Sequence 5302, Ap	985	39.5	8.6	254	7	US-11-067-323-440	Sequence 440, App
913	39.5	8.6	221	6	US-10-467-657-3194	Sequence 3194, Ap	986	39.5	8.6	254	7	US-11-067-323-448	Sequence 448, App
914	39.5	8.6	223	6	US-11-112-882-88	Sequence 88, Appl	987	39.5	8.6	254	7	US-11-067-323-452	Sequence 452, App
915	39.5	8.6	225	6	US-10-467-657-5214	Sequence 5214, Ap	988	39.5	8.6	254	7	US-11-067-323-454	Sequence 454, App
916	39.5	8.6	230	6	US-10-510-386-198	Sequence 198, App	989	39.5	8.6	254	7	US-11-067-323-456	Sequence 456, App
917	39.5	8.6	230	7	US-11-080-628-24	Sequence 24, Appl	990	39.5	8.6	254	7	US-11-067-323-458	Sequence 458, App
918	39.5	8.6	236	7	US-11-000-463-390	Sequence 390, App	991	39.5	8.6	254	7	US-11-067-323-470	Sequence 470, App
919	39.5	8.6	237	6	US-10-793-626-162	Sequence 162, App	992	39.5	8.6	254	7	US-11-067-323-472	Sequence 472, App
920	39.5	8.6	246	6	US-10-878-556A-194	Sequence 194, App	993	39.5	8.6	254	7	US-11-067-323-476	Sequence 476, App
921	39.5	8.6	252	6	US-10-821-234-1193	Sequence 1193, Ap	994	39.5	8.6	254	7	US-11-067-323-490	Sequence 490, App
922	39.5	8.6	252	7	US-11-067-323-18	Sequence 18, Appl	995	39.5	8.6	254	7	US-11-067-323-492	Sequence 492, App
923	39.5	8.6	252	7	US-11-067-323-28	Sequence 28, Appl	996	39.5	8.6	254	7	US-11-067-323-494	Sequence 494, App
924	39.5	8.6	253	6	US-10-821-234-1438	Sequence 2, Appl1	997	39.5	8.6	254	7	US-11-067-323-500	Sequence 500, App
925	39.5	8.6	254	7	US-11-067-323-2	Sequence 2, Appl1	998	39.5	8.6	254	7	US-11-067-323-502	Sequence 502, App
926	39.5	8.6	254	7	US-11-067-323-4	Sequence 4, Appl1	999	39.5	8.6	254	7	US-11-067-323-508	Sequence 508, App
927	39.5	8.6	254	7	US-11-067-323-6	Sequence 6, Appl1	1000	39.5	8.6	254	7	US-11-067-323-512	Sequence 512, App
928	39.5	8.6	254	7	US-11-067-323-8	Sequence 8, Appl1	1001	39.5	8.6	254	7	US-11-067-323-514	Sequence 514, App
929	39.5	8.6	254	7	US-11-067-323-10	Sequence 10, Appl1	1002	39.5	8.6	254	7	US-11-067-323-516	Sequence 516, App

1003	39.5	8.6	254	7	US-11-067-323-528	Sequence 528, App	1076	39.5	8.6	404	6	US-10-793-626-1204	Sequence 1204, Ap
1004	39.5	8.6	254	7	US-11-067-323-530	Sequence 530, App	1077	39.5	8.6	410	6	US-10-858-730-233	Sequence 233, App
1005	39.5	8.6	254	7	US-11-067-323-532	Sequence 532, App	1078	39.5	8.6	413	6	US-11-060-029-4	Sequence 4, Appl1
1006	39.5	8.6	254	7	US-11-067-323-534	Sequence 534, App	1079	39.5	8.6	445	7	US-11-000-463-461	Sequence 461, App
1007	39.5	8.6	254	7	US-11-067-323-552	Sequence 552, App	1080	39.5	8.6	445	7	US-10-793-626-2928	Sequence 2228, Ap
1008	39.5	8.6	254	7	US-11-067-323-554	Sequence 554, App	1081	39.5	8.6	478	7	US-11-054-385-8	Sequence 8, Appl1
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1011	39.5	8.6	254	7	US-11-067-323-570	Sequence 570, App	1084	39.5	8.6	528	6	US-10-858-730-89	Sequence 89, Appl1
1012	39.5	8.6	254	7	US-11-067-323-572	Sequence 572, App	1085	39.5	8.6	564	6	US-10-485-517-253	Sequence 253, App
1013	39.5	8.6	254	7	US-11-067-323-576	Sequence 576, App	1086	39.5	8.6	564	6	US-10-485-517-290	Sequence 290, App
1014	39.5	8.6	254	7	US-11-067-323-578	Sequence 578, App	1087	39.5	8.6	587	6	US-10-925-970-6	Sequence 6, Appl1
1015	39.5	8.6	254	7	US-11-067-323-580	Sequence 580, App	1088	39.5	8.6	648	6	US-10-467-657-7802	Sequence 2802, Ap
1016	39.5	8.6	254	7	US-11-067-323-582	Sequence 582, App	1089	39.5	8.6	686	7	US-11-113-424-46	Sequence 46, Appl1
1017	39.5	8.6	254	7	US-11-067-323-584	Sequence 584, App	1090	39.5	8.6	696	7	US-11-029-003-8	Sequence 8, Appl1
1018	39.5	8.6	254	7	US-11-067-323-598	Sequence 598, App	1091	39.5	8.6	753	6	US-10-858-730-225	Sequence 225, App
1019	39.5	8.6	254	7	US-11-067-323-620	Sequence 620, App	1092	39.5	8.6	794	6	US-10-793-626-1050	Sequence 1050, Ap
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1021	39.5	8.6	254	7	US-11-067-323-624	Sequence 624, App	1094	39.5	8.6	858	6	US-10-645-441-18	Sequence 18, Appl1
1022	39.5	8.6	254	7	US-11-067-323-640	Sequence 640, App	1095	39.5	8.6	858	6	US-10-645-441-20	Sequence 20, Appl1
1023	39.5	8.6	254	7	US-11-067-323-642	Sequence 642, App	1096	39.5	8.6	858	6	US-10-645-441-23	Sequence 23, Appl1
1024	39.5	8.6	254	7	US-11-067-323-644	Sequence 644, App	1097	39.5	8.6	859	7	US-11-000-463-423	Sequence 423, App
1025	39.5	8.6	254	7	US-11-067-323-646	Sequence 646, App	1098	39.5	8.6	859	7	US-11-000-463-895	Sequence 895, App
1026	39.5	8.6	254	7	US-11-067-323-648	Sequence 648, App	1099	39.5	8.6	898	7	US-11-174-150-43	Sequence 43, Appl1
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1028	39.5	8.6	254	7	US-11-067-323-684	Sequence 684, App	1101	39.5	8.6	1049	6	US-10-392-234A-12	Sequence 12, Appl1
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1032	39.5	8.6	254	7	US-11-067-323-692	Sequence 692, App	1105	39.5	8.6	1198	6	US-10-451-375-4	Sequence 4, Appl1
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1035	39.5	8.6	254	7	US-11-067-323-698	Sequence 698, App	1108	39.5	8.6	3073	6	US-10-467-657-6322	Sequence 6322, App
1036	39.5	8.6	254	7	US-11-067-323-700	Sequence 700, App	1109	39.5	8.6	3690	6	US-11-143-980-50	Sequence 50, Appl1
1037	39.5	8.6	254	7	US-11-067-323-704	Sequence 704, App	1110	39.5	8.6	3714	6	US-10-995-561-1015	Sequence 1015, Ap
1038	39.5	8.6	254	7	US-11-067-323-706	Sequence 706, App	1111	39.5	8.6	3717	6	US-10-821-234-1076	Sequence 1076, Ap
1039	39.5	8.6	254	7	US-11-067-323-708	Sequence 708, App	1112	39.5	8.6	43	6	US-10-957-8878-222	Sequence 1276, Ap
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1042	39.5	8.6	254	7	US-11-067-323-714	Sequence 714, App	1115	39	8.5	86	7	US-11-055-822-3	Sequence 52, Appl1
1043	39.5	8.6	254	7	US-11-067-323-716	Sequence 716, App	1116	39	8.5	90	7	US-11-053-076-52	Sequence 5070, App
1044	39.5	8.6	254	7	US-11-067-323-720	Sequence 720, App	1117	39	8.5	98	7	US-11-084-554-220	Sequence 520, App
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1047	39.5	8.6	254	7	US-11-067-323-740	Sequence 740, App	1120	39	8.5	105	7	US-11-074-176-144	Sequence 178, App
1048	39.5	8.6	254	7	US-11-067-323-742	Sequence 742, App	1121	39	8.5	107	7	US-11-082-544-12	Sequence 630, Ap
1049	39.5	8.6	266	6	US-10-884-730-345	Sequence 345, App	1122	39	8.5	108	7	US-11-082-544-12	Sequence 294, App
1050	39.5	8.6	273	6	US-10-793-626-728	Sequence 728, App	1123	39	8.5	122	7	US-11-074-176-144	Sequence 12, Appl1
1051	39.5	8.6	273	6	US-10-467-657-7792	Sequence 7792, App	1124	39	8.5	129	6	US-11-092-140-30	Sequence 30, Appl1
1052	39.5	8.6	280	6	US-10-967-457-75	Sequence 75, Appl1	1125	39	8.5	131	7	US-11-082-517-178	Sequence 178, App
1053	39.5	8.6	296	6	US-10-467-657-3198	Sequence 3198, App	1126	39	8.5	132	6	US-11-062-186-65	Sequence 6530, Ap
1054	39.5	8.6	304	7	US-11-055-822-108	Sequence 108, App	1127	39	8.5	139	7	US-11-082-389-294	Sequence 294, App
1055	39.5	8.6	319	7	US-11-184-005-8	Sequence 8, Appl1	1128	39	8.5	154	7	US-11-082-544-12	Sequence 12, Appl1
1056	39.5	8.6	322	6	US-10-467-657-3484	Sequence 3484, Ap	1129	39	8.5	156	7	US-11-055-822-744	Sequence 744, App
1057	39.5	8.6	334	6	US-10-858-730-114	Sequence 114, App	1130	39	8.5	162	6	US-10-467-657-7062	Sequence 7062, Ap
1058	39.5	8.6	338	6	US-10-821-234-1565	Sequence 1565, Ap	1131	39	8.5	184	7	US-11-084-591-5	Sequence 5, Appl1
1059	39.5	8.6	341	6	US-10-793-626-1188	Sequence 1188, Ap	1132	39	8.5	188	7	US-11-194-246-292	Sequence 292, App
1060	39.5	8.6	354	6	US-10-821-234-1618	Sequence 1618, Ap	1133	39	8.5	204	7	US-11-062-471A-1	Sequence 1, Appl1
1061	39.5	8.6	358	6	US-10-980-388-96	Sequence 96, Appl1	1134	39	8.5	204	7	US-11-062-471A-1	Sequence 2, Appl1
1062	39.5	8.6	360	6	US-10-467-657-75	Sequence 75, Appl1	1135	39	8.5	205	6	US-10-793-626-202	Sequence 202, App
1063	39.5	8.6	367	6	US-10-793-626-1202	Sequence 1202, Ap	1136	39	8.5	207	6	US-10-858-730-196	Sequence 196, App
1064	39.5	8.6	369	6	US-10-432-483-18	Sequence 18, Appl1	1137	39	8.5	224	6	US-10-467-657-5378	Sequence 5378, Ap
1065	39.5	8.6	373	7	US-11-082-389-248	Sequence 248, App	1138	39	8.5	225	6	US-10-467-657-26	Sequence 26, Appl1
1066	39.5	8.6	380	6	US-10-793-626-1402	Sequence 1402, App	1139	39	8.5	227	6	US-10-467-657-1514	Sequence 1514, Ap
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1068	39.5	8.6	389	6	US-10-980-388-116	Sequence 116, App	1141	39	8.5	240	6	US-10-467-657-7890	Sequence 7890, Ap
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1071	39.5	8.6	389	7	US-11-060-008-11	Sequence 11, Appl1	1144	39	8.5	246	7	US-11-067-121-13	Sequence 13, Appl1
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1073	39.5	8.6	394	6	US-10-821-234-1187	Sequence 1187, Ap	1146	39	8.5	251	7	US-11-054-515-1133	Sequence 1133, Ap
1074	39.5	8.6	397	6	US-10-467-657-3944	Sequence 3944, Ap	1147	39	8.5	252	7	US-11-054-515-1021	Sequence 1021, Ap
1075	39.5	8.6	400	6	US-10-467-657-7428	Sequence 7428, Ap	1148	39	8.5	252	7	US-11-054-515-1218	Sequence 1218, Ap

1295	39	8.5	254	7	US-11-067-323-1015	Sequence 1015, Ap	1368	39	8.5	359	7	US-11-108-528-62	Sequence 62, Appl
1296	39	8.5	254	7	US-11-067-323-1017	Sequence 1017, Ap	1369	39	8.5	375	7	US-11-051-267-16	Sequence 16, Appl
1297	39	8.5	254	7	US-11-067-323-1021	Sequence 1021, Ap	1370	39	8.5	387	7	US-11-092-140-17	Sequence 17, Appl
1298	39	8.5	254	7	US-11-067-323-1023	Sequence 1023, Ap	1371	39	8.5	389	6	US-10-793-626-118	Sequence 68, Appl
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probable proline-s
potassium channel
potassium channel
voltage-gated pota
phosphoribosylform
vitellinogen B1 pr
paired box protein
type 4 preplilin pe
transcription fact
hypothetical prote
membrane protein L
hypothetical 60.6
HC-toxin synthetas
phosphomethylpyrim
amino acid ABC tra
occlusion-derived
glucose transport
probable hexose tr
unknown protein en
NADH2 dehydrogenas
probable NAD(P)H c
probable channel p
probable membrane
integral membrane
3-oxoacyl-l-acyl-ca
permease (imported
probable sugar upt
NADH2 dehydrogenas
glycerol 3 phospho
potassium channel
potassium channel
potassium channel
potassium channel
potassium channel
potassium channel
potassium channel
proline/betaine tr
proline/betaine tr
potassium channel
probable transport
potassium channel
potassium channel
delayed rectifier
conserved hypothet
hypothetical prote
hypothetical prote
transcription regu
potassium channel
Shaw type potassi
leucine-cRNA ligas
GGDEF family prote

103	58	12.6	185	2	AG1054	probable exported
104	58	12.6	196	2	E75612	hypothetical prote
105	58	12.6	215	2	AF0650	probable membrane
106	58	12.6	257	2	A64459	diphthine synthase
107	58	12.6	277	2	S44252	raffinose operon r
108	58	12.6	368	2	T26425	hypothetical prote
109	58	12.6	376	2	AH1795	hypothetical membr
110	58	12.6	398	2	A82081	cell division prot
111	58	12.6	462	2	F75588	probable kynurenin
112	58	12.6	4836	2	T14346	hcr2c protein - mo
113	57.5	12.5	71	2	D23876	vitellinogen B2 pr
114	57.5	12.5	139	2	AF0685	hypothetical prote
115	57.5	12.5	324	2	T36805	conserved hypotnet
116	57.5	12.5	342	2	A47673	photosystem II chl
117	57.5	12.5	356	2	C72475	hypothetical prote
118	57.5	12.5	374	2	T10415	virus envelope pro
119	57.5	12.5	461	2	B83601	C4-dicarboxylate a
120	57.5	12.5	461	2	AF0579	probable transport
121	57.5	12.5	523	2	B83629	probable ATP-bindi
122	57.5	12.5	528	2	T14205	potassium channel
123	57.5	12.5	594	2	B90586	gene F protein - r
124	57.5	12.5	636	2	S47299	hypothetical prote
125	57.5	12.5	662	2	T44034	hypothetical prote
126	57.5	12.5	662	2	T44034	lactocepin (EC 3.4
127	57.5	12.5	1902	1	B44858	probable membrane
128	57	12.4	148	2	C84690	adenomedullin pre
129	57	12.4	185	2	UN0766	probable uridine p
130	57	12.4	258	2	F71251	hypothetical prote
131	57	12.4	269	2	AG2268	iron stress-induce
132	57	12.4	342	2	A30189	nodulin-like prote
133	57	12.4	374	2	T00561	hypothetical prote
134	57	12.4	385	2	T04725	hypothetical prote
135	57	12.4	440	2	H86312	F2h15.2 protein -
136	57	12.4	456	2	H86902	membrane protein,
137	57	12.4	457	2	B64768	proline transport
138	57	12.4	457	2	B64768	proline permease t
139	57	12.4	457	2	D90685	proline permease t
140	57	12.4	457	2	H85535	c4-dicarboxylate a
141	57	12.4	461	2	D90711	danc protein - Bac
142	57	12.4	461	2	C64796	transport of dicar
143	57	12.4	461	2	H85561	photoystem II 44k
144	57	12.4	487	2	S73277	homeotic protein R
145	56.5	12.3	114	2	E43559	21k protein - Shlg
146	56.5	12.3	187	2	S70186	probable exported
147	56.5	12.3	191	2	AD0905	probable lipoprote
148	56.5	12.3	233	2	F70668	uridine phosphoryl
149	56.5	12.3	258	2	D84336	potassium channel
150	56.5	12.3	361	2	S19552	endothelapepsin (EC
151	56.5	12.3	419	2	S42136	hypothetical prote
152	56.5	12.3	471	2	T04911	potassium uptake p
153	56.5	12.3	485	2	E97506	spovB related memb
154	56.5	12.3	500	2	F97025	Na+/H+ antiporter
155	56.5	12.3	614	2	A69845	conserved hypotnet
156	56.5	12.3	670	1	E70040	glycoprotein H pre
157	56.5	12.3	686	1	VBENK	glycoprotein H - s
158	56.5	12.3	686	1	VBENK	glycoprotein H - s
159	56.5	12.3	686	2	S15478	hypothetical prote
160	56.5	12.3	852	2	S25359	hypothetical prote
161	56	12.1	79	1	TREPVK	K+ channel blocker
162	56	12.1	196	2	E64231	hypothetical prote
163	56	12.1	222	2	F82353	conserved hypotnet
164	56	12.1	261	2	AB2966	conserved hypotnet
165	56	12.1	261	2	B98317	ATP synthase chain
166	56	12.1	388	2	T09885	hypothetical prote
167	56	12.1	411	2	C87586	metal ion efflux m
168	56	12.1	436	2	G70058	hypothetical prote
169	56	12.1	440	2	C97376	probable transport
170	56	12.1	440	2	A12593	MPS permease [impo
171	56	12.1	449	2	H70546	hypothetical prote
172	56	12.1	503	2	S36514	LI protein - human
173	56	12.1	547	2	D95337	probable manganese
174	56	12.1	558	2	S29125	dimethylamline mo
175	56	12.1	578	2	B37852	phosphotransferase
176	56	12.1	594	2	A83096	probable permease
177	56	12.1	626	2	D70178	Pis system, fructo
178	56	12.1	736	2	C69451	cationic amino aci
179	56	12.1	1118	2	C95385	probable adenylate
180	56	12.1	1305	2	AB0168	probable cell divi
181	56	12.1	2055	2	T30259	multiple PDZ domai
182	56	12.1	3329	2	T42205	breast cancer susc
183	56	12.1	5170	2	T15348	hypothetical prote
184	55.5	12.0	245	2	A90521	hypothetical prote
185	55.5	12.0	249	4	T44821	bacteriorhodopsin
186	55.5	12.0	254	2	F75496	conserved hypotnet
187	55.5	12.0	256	2	E75401	hypothetical prote
188	55.5	12.0	259	4	T44820	bacteriorhodopsin
189	55.5	12.0	262	1	RAHSB	bacteriorhodopsin
190	55.5	12.0	262	2	H84300	pancreatic elastase
191	55.5	12.0	270	2	B29934	hypothetical prote
192	55.5	12.0	299	2	B83243	legatose-6-phospha
193	55.5	12.0	309	2	C95138	hypothetical prote
194	55.5	12.0	309	2	A98006	exoz protein - Rhi
195	55.5	12.0	316	2	G75388	acetyltransferase
196	55.5	12.0	317	2	S16299	photosystem II chl
197	55.5	12.0	317	2	B95975	photosystem II chl
198	55.5	12.0	344	2	S42648	photosystem II chl
199	55.5	12.0	344	2	AB2306	photosystem II chl
200	55.5	12.0	346	2	C71042	probable chreonine
201	55.5	12.0	376	2	F72868	occlusion-derived
202	55.5	12.0	383	2	S53379	probable membrane
203	55.5	12.0	385	2	F86464	hypothetical prote
204	55.5	12.0	389	2	B81347	probable aspartate
205	55.5	12.0	456	2	T22347	hypothetical prote
206	55.5	12.0	459	2	D86669	amino acid permeas
207	55.5	12.0	545	2	A12337	hypothetical prote
208	55.5	12.0	609	2	S28283	hypothetical prote
209	55.5	12.0	625	2	S13919	potassium channel
210	55.5	12.0	648	2	C71658	probable primosoma
211	55.5	12.0	716	2	T03635	delta 1 pyroline-
212	55.5	12.0	851	2	T12503	hypothetical prote
213	55.5	12.0	946	1	A29550	methylenetetrahydr
214	55.5	12.0	1217	2	T22672	hypothetical prote
215	55.5	12.0	1423	2	A49206	exo-beta-D-fructos
216	55.5	12.0	2054	2	T46652	multi PDZ domain p
217	55	11.9	52	2	T32956	hypothetical prote
218	55	11.9	52	2	T33694	hypothetical prote
219	55	11.9	128	2	F71371	hypothetical prote
220	55	11.9	169	2	S18653	hypothetical prote
221	55	11.9	212	2	E82135	conserved hypotnet
222	55	11.9	268	2	S05471	embryonic abundant
223	55	11.9	268	2	S14068	seed protein precu
224	55	11.9	288	2	T12462	hypothetical prote
225	55	11.9	312	2	B75405	endopeptidase-rela
226	55	11.9	334	2	S54438	hemin permease [va
227	55	11.9	336	2	AH0201	probable zinc-bind
228	55	11.9	340	2	AF2896	hypothetical prote
229	55	11.9	340	2	H97671	hypothetical prote
230	55	11.9	344	2	E84043	glyceraledehyde-3-p
231	55	11.9	357	2	A23641	R2 protein, testis
232	55	11.9	376	1	S17246	cholesterol synthas
233	55	11.9	404	2	S34031	KRM3 protein - Yea
234	55	11.9	410	2	AH2895	hypothetical prote
235	55	11.9	410	2	C97671	probable maltose-b
236	55	11.9	443	2	B86180	protein Y1G11.3 [i
237	55	11.9	459	2	A87201	conserved hypotnet
238	55	11.9	461	2	S57713	probable mannosyl
239	55	11.9	473	1	F2K4C	photosystem II chl
240	55	11.9	482	2	AG1147	P60 extracellular
241	55	11.9	484	2	A41467	protein P60 precu
242	55	11.9	654	2	A96235	hydroxamate-depend
243	55	11.9	654	2	AC3051	hypothetical prote
244	55	11.9	716	2	E69672	penicillin-binding
245	55	11.9	2531	2	S18188	notch protein homo
246	55	11.9	2531	2	A46019	notch-1 protein -
247	54.5	11.8	173	2	S33295	translocon-associa
248	54.5	11.8	177	2	G75285	hypothetical prote

249	54.5	11.8	185	2	T51844	RING-H2 finger pro	322	54	11.7	909	2	T00009	probable primase (
250	54.5	11.8	204	2	AC1961	ATP-dependent Clp	323	54	11.7	967	2	I40889	sarcosine oxidase
251	54.5	11.8	226	2	S76020	endopeptidase Clp	324	54	11.7	993	2	A38437	probable homeotic
252	54.5	11.8	255	2	F86203	hypothetical prote	325	54	11.7	1072	2	T50949	veprolin related
253	54.5	11.8	269	2	T19947	hypothetical prote	326	54	11.7	1222	2	G72614	probable reverse g
254	54.5	11.8	276	2	AC1838	hypothetical prote	327	54	11.7	1283	2	T18939	hypothetical prote
255	54.5	11.8	282	2	PQ0376	cell fusion glycop	328	53.5	11.6	114	2	C90344	hypothetical prote
256	54.5	11.8	296	2	F83145	probable epoxide h	329	53.5	11.6	153	2	T49895	oleosin-like prote
257	54.5	11.8	296	2	A85698	transposase for IS	330	53.5	11.6	173	2	S01145	hypothetical prote
258	54.5	11.8	296	2	A99840	transposase for IS	331	53.5	11.6	211	2	G82573	CDP-diacylglycerol
259	54.5	11.8	304	2	S59965	phosphotransferase	332	53.5	11.6	225	1	CYRGE	epsilon-crystallin
260	54.5	11.8	337	2	G87487	conserved hypothet	333	53.5	11.6	269	2	D6957	uncharacterized me
261	54.5	11.8	362	2	S77244	biotin synthase (E	334	53.5	11.6	282	2	PQ0388	cell fusion glycop
262	54.5	11.8	369	2	E83122	hypothetical prote	335	53.5	11.6	296	2	C90978	IS629 transposase
263	54.5	11.8	373	2	G85355	nodulin-like prote	336	53.5	11.6	296	2	H85824	IS629 transposase
264	54.5	11.8	393	2	AB0035	cyathionine beta	337	53.5	11.6	303	2	T13598	trypsin homolog -
265	54.5	11.8	422	2	T07967	mandelonitrile lya	338	53.5	11.6	307	2	B87292	conserved hypothet
266	54.5	11.8	445	1	S54140	D-serine permease	339	53.5	11.6	339	2	H71265	hypothetical prote
267	54.5	11.8	458	1	Y7BSRT	tetracycline resis	340	53.5	11.6	346	2	D70558	probable cyd8 prot
268	54.5	11.8	458	1	Y7SOG	tetracycline resis	341	53.5	11.6	357	2	F81679	chorismate synthas
269	54.5	11.8	458	1	Y7BSU6	tetracycline resis	342	53.5	11.6	376	2	AF1943	multidrug-efflux t
270	54.5	11.8	458	2	Y01211	tetracycline resis	343	53.5	11.6	378	2	T34372	hypothetical prote
271	54.5	11.8	458	2	S23743	tetracycline resis	344	53.5	11.6	383	2	T48018	hypothetical prote
272	54.5	11.8	483	1	A53595	allantoicase (EC 3	345	53.5	11.6	410	2	A48585	transcription fact
273	54.5	11.8	484	2	T00158	amidase (EC 3.5.-	346	53.5	11.6	412	2	AH3274	phycosystem II chl
274	54.5	11.8	501	2	E87239	aldehyde dehydroge	347	53.5	11.6	461	2	T06936	potassium channel
275	54.5	11.8	576	2	A49933	protease SM tran	348	53.5	11.6	495	2	I57680	potassium channel
276	54.5	11.8	586	2	T48672	ABC-type transport	349	53.5	11.6	495	2	A40090	potassium channel
277	54.5	11.8	622	2	AC1236	acylttransferase (t	350	53.5	11.6	495	2	B39113	hypothetical prote
278	54.5	11.8	628	2	T01467	hypothetical prote	351	53.5	11.6	529	2	H84049	hypothetical prote
279	54.5	11.8	722	2	B71728	probable peptidase	352	53.5	11.6	539	2	T32693	hypothetical prote
280	54.5	11.8	735	2	E69139	hypothetical prote	353	53.5	11.6	546	2	S47300	gene F protein - r
281	54.5	11.8	895	2	I54343	dysferlin-like - hm	354	53.5	11.6	553	1	VGNZWV	cell fusion glycop
282	54.5	11.8	895	2	S20582	dysferlin-like - hm	355	53.5	11.6	556	2	T03114	segment protein -
283	54.5	11.8	900	2	G87431	pyruvate phosphate	356	53.5	11.6	571	1	H65169	probable transport
284	54.5	11.8	1044	2	AB2158	heterocyst differe	357	53.5	11.6	571	2	D91206	probable cotranspo
285	54.5	11.8	1044	2	AB2158	heterocyst differe	358	53.5	11.6	571	2	F86052	probable cotranspo
286	54.5	11.8	1099	2	T14850	S-layer protein pr	359	53.5	11.6	594	2	T43246	amino acid transpo
287	54.5	11.8	1146	2	B35962	protein-tyrosine k	360	53.5	11.6	597	2	AH2351	serine/threonine k
288	54.5	11.8	1182	2	A35962	protein-tyrosine k	361	53.5	11.6	890	2	T35237	probable secreted
289	54	11.7	98	2	T17183	NADH2 dehydrogenas	362	53.5	11.6	945	2	S30398	aminopeptidase N h
290	54	11.7	98	2	T17183	NADH2 dehydrogenas	363	53.5	11.6	985	2	T10339	DNA-directed DNA p
291	54	11.7	154	1	MMBE16	16.9K membrane pro	364	53.5	11.6	1045	2	E90705	hypothetical prote
292	54	11.7	168	2	S47881	NADH2 dehydrogenas	365	53.5	11.6	1045	2	H85555	hypothetical prote
293	54	11.7	188	2	A75382	hypothetical prote	366	53.5	11.6	1047	2	E64790	YbdE protein - Bac
294	54	11.7	248	1	PRM5C2	granzyme C (EC 3.4	367	53.5	11.6	1075	2	S76432	cation efflux syst
295	54	11.7	259	2	C64481	conserved hypothet	368	53.5	11.6	1175	2	S51005	protein-tyrosine-p
296	54	11.7	292	2	T14627	hypothetical prote	369	53.5	11.6	2037	2	T16881	hypothetical prote
297	54	11.7	316	2	F91044	transaldolase A (I	370	53.5	11.6	3566	1	A40701	tenascin-X precurs
298	54	11.7	316	2	A85889	transaldolase A (I	371	53	11.5	90	2	T33692	similar to avrRpt2
299	54	11.7	316	2	G65021	transaldolase (EC	372	53	11.5	148	2	A84636	hypothetical prote
300	54	11.7	328	2	A69218	hypothetical prote	373	53	11.5	154	1	F70002	conserved hypothet
301	54	11.7	346	2	C86413	cysteine proteinas	374	53	11.5	166	2	D58889	NADH2 dehydrogenas
302	54	11.7	351	2	I68620	rod outer segment	375	53	11.5	201	2	A71124	hypothetical prote
303	54	11.7	356	2	S66348	cysteine proteinas	376	53	11.5	202	2	JC6205	cell surface anti g
304	54	11.7	356	2	B97742	hypothetical prote	377	53	11.5	210	2	JC5448	serine protease
305	54	11.7	386	2	F69061	hypothetical prote	378	53	11.5	214	2	AH0265	small neutral amin
306	54	11.7	386	2	A72313	hypothetical prote	379	53	11.5	216	2	UC7930	beta-tubulin ASL1
307	54	11.7	394	2	C64185	cell division prot	380	53	11.5	224	2	S67949	beta-tubulin ASL1
308	54	11.7	428	2	S08084	gene IV protein -	381	53	11.5	224	2	S73823	MG243 homolog H91
309	54	11.7	440	2	E84118	UDP-N-acetylglucos	382	53	11.5	257	2	D71544	hypothetical prote
310	54	11.7	456	2	TA00551	proline-specific p	383	53	11.5	264	2	A75076	membrane protein p
311	54	11.7	476	2	T40086	hypothetical prote	384	53	11.5	279	2	A95933	probable inositol
312	54	11.7	549	2	C86692	peptide-binding pr	385	53	11.5	300	2	B83100	inhibitor of chrom
313	54	11.7	573	2	AE1236	glycerol 3 phosph	386	53	11.5	306	2	D88040	protein P47F6.1 (I
314	54	11.7	573	1	S33212	IND1 protein - fu	387	53	11.5	310	2	D87704	integral membrane
315	54	11.7	604	2	B84221	hypothetical prote	388	53	11.5	339	2	AC0165	L-allo-threonine a
316	54	11.7	625	2	T25373	hypothetical prote	389	53	11.5	342	2	A44965	cysteine proteinas
317	54	11.7	634	2	T33528	hypothetical prote	390	53	11.5	342	2	A45524	antirrhizate phosph
318	54	11.7	787	2	T38224	probable glycosyl	391	53	11.5	364	2	AH1857	antirrhizate phosph
319	54	11.7	869	2	A96558	probable protein k	392	53	11.5	376	2	B95879	probable sugar ABC
320	54	11.7	880	2	S49627	regulatory protein	393	53	11.5	377	2	A53044	geranylgeranyl-dip
321	54	11.7	885	2	G83260	aminopeptidase N p	394	53	11.5	385	2	A91178	probable membrane

395	53	11.5	385	2	B86024	probable membrane	468	52.5	11.4	409	2	T47644	protein phosphatase
396	53	11.5	385	2	S47733	gamma protein precursor	469	52.5	11.4	410	2	B48585	transcription factor
397	53	11.5	385	2	A26017	patatin T5 precursor	470	52.5	11.4	421	2	T35515	hypothetical protein
398	53	11.5	403	2	E69873	cell-division protein	471	52.5	11.4	422	2	JE0239	11n-10 protein - r
399	53	11.5	405	2	S61551	breast-regressing	472	52.5	11.4	422	2	E82904	hypothetical protein
400	53	11.5	409	2	P83483	probable MFS trans	473	52.5	11.4	429	2	AF0681	probable voltage g
401	53	11.5	418	2	H82087	MPC family protein	474	52.5	11.4	429	2	S30049	transcription factor
402	53	11.5	426	2	B82712	ATP-dependent Clp	475	52.5	11.4	452	2	G95356	probable oxidoredu
403	53	11.5	438	2	H86575	arylesterase-relat	476	52.5	11.4	500	2	H70629	probable AMINOPEPT
404	53	11.5	447	2	H86534	hypothetical protein	477	52.5	11.4	514	2	T21286	hypothetical protein
405	53	11.5	447	2	H72089	hypothetical protein	478	52.5	11.4	523	2	S51401	probable membrane
406	53	11.5	463	2	B81580	hypothetical protein	479	52.5	11.4	533	1	VRM5CS	monophenol monooxy
407	53	11.5	469	1	AJEBQT	glutamate-ammoma	480	52.5	11.4	542	2	AH2191	hypothetical protein
408	53	11.5	469	2	A10949	glutamate syntheta	481	52.5	11.4	542	2	A13564	hypothetical membr
409	53	11.5	469	2	S23899	glutamate-ammoma	482	52.5	11.4	546	2	B32688	beta-galactosidase
410	53	11.5	471	2	S78347	phosphorylase II chl	483	52.5	11.4	549	2	G91178	cytoplasmic trehal
411	53	11.5	515	2	B84406	TPK potassium upa	484	52.5	11.4	549	2	H86024	cytoplasmic trehal
412	53	11.5	581	2	T38501	hypothetical protein	485	52.5	11.4	549	2	S47739	probable alpha,alp
413	53	11.5	588	2	T20036	hypothetical protein	486	52.5	11.4	572	2	A55676	excitatory amino a
414	53	11.5	588	2	AC2276	oligopeptide bindi	487	52.5	11.4	652	2	AH2245	2',3'-cyclic-nucle
415	53	11.5	605	2	E69153	cadmium efflux ATP	488	52.5	11.4	657	1	A64079	hypothetical protein
416	53	11.5	610	2	A55939	dihydrofolipamide S	489	52.5	11.4	666	2	T06700	NADH2 dehydrogenas
417	53	11.5	618	2	A13303	hypothetical protein	490	52.5	11.4	699	2	T12170	NADH2 dehydrogenas
418	53	11.5	637	2	T49099	diacylglycerolamid	491	52.5	11.4	699	2	T12172	NADH2 dehydrogenas
419	53	11.5	653	2	A83154	probable choline t	492	52.5	11.4	699	2	T12173	NADH2 dehydrogenas
420	53	11.5	656	2	T52064	dnaf-like protein	493	52.5	11.4	795	1	SYECFB	phenylalanine-cRNA
421	53	11.5	728	2	D86278	hypothetical protein	494	52.5	11.4	795	1	H85779	phenylalanine-cRNA
422	53	11.5	770	2	T23999	hypothetical protein	495	52.5	11.4	795	2	D90931	phenylalanine cRNA
423	53	11.5	776	2	T02584	probable protein k	496	52.5	11.4	803	2	F83360	glucose dehydrogen
424	53	11.5	1005	2	B82969	barcosine oxidase	497	52.5	11.4	826	2	E90289	malate synthase, p
425	53	11.5	1070	2	UC4593	protein-tyrosine k	498	52.5	11.4	883	2	AE0207	conserved hypotnet
426	53	11.5	1162	2	E84431	probable Na+/H+ an	499	52.5	11.4	977	2	T41289	hypothetical protein
427	53	11.5	1176	2	E15835	protein tyrosine p	500	52.5	11.4	1011	2	T40851	hypothetical protein
428	53	11.5	1240	1	DJBE21	DNA-directed DNA p	501	52.5	11.4	1205	2	T18517	hypothetical protein
429	53	11.5	1250	2	T00454	hypothetical protein	502	52.5	11.4	1225	1	S24284	E2 glycoprotein pr
430	53	11.5	1305	2	T23314	hypothetical protein	503	52.5	11.4	1225	1	A36607	major capsid prote
431	53	11.5	1326	2	B63935	secretory phosphol	504	52.5	11.4	1345	1	VCBEH6	spike protein - ca
432	53	11.5	1331	2	S05011	calcium channel al	505	52.5	11.4	1453	2	S41453	pilocarpate-incorpo
433	53	11.5	1465	2	A56395	secretory phosphol	506	52.5	11.4	1541	2	T30227	hypothetical protein
434	53	11.5	1529	2	T16779	hypothetical prote	507	52.5	11.4	1544	2	T29482	DNA-directed DNA p
435	53	11.5	2143	2	JH0427	voltage-dependent	508	52.5	11.4	2285	1	G02434	hypothetical protein
436	53	11.5	2166	2	S11339	calcium channel pr	509	52	11.3	119	2	D64611	hypothetical prote
437	53	11.5	2171	2	S05054	calcium channel al	510	52	11.3	122	2	F75351	hypothetical prote
438	53	11.5	2599	2	A96616	unknown protein F1	511	52	11.3	148	2	D64356	conserved hypotnet
439	52.5	11.4	71	2	I50433	vitellinogen III -	512	52	11.3	160	2	G95113	regulatory protein
440	52.5	11.4	78	2	G64339	hypothetical protein	513	52	11.3	160	2	H97982	hypothetical protein
441	52.5	11.4	159	2	B85360	ribosomal protein	514	52	11.3	175	2	AE1508	hypothetical prote
442	52.5	11.4	165	2	C72116	hypothetical protein	515	52	11.3	202	2	UC4635	tumor-associated L
443	52.5	11.4	210	2	A83516	probable outer mem	516	52	11.3	207	2	T45600	hypothetical prote
444	52.5	11.4	219	2	F75402	probable competenc	517	52	11.3	219	2	G97271	probable phosphogl
445	52.5	11.4	219	2	AC1881	hypothetical prote	518	52	11.3	235	2	E82173	pseudouridine synt
446	52.5	11.4	244	2	S29982	class II histocomp	519	52	11.3	238	2	C82866	conjugal transfer
447	52.5	11.4	245	2	S29980	class II histocomp	520	52	11.3	260	2	I56559	neuropain - mouse
448	52.5	11.4	256	2	S14518	chlorophyll a/b-bi	521	52	11.3	262	2	B81200	conserved hypotnet
449	52.5	11.4	257	2	S29981	class II histocomp	522	52	11.3	265	2	D83761	hypothetical prote
450	52.5	11.4	285	1	A43556	homeotic protein H	523	52	11.3	291	2	B75618	chromosome partiti
451	52.5	11.4	289	1	E64330	dihydrodipicolinat	524	52	11.3	295	2	E85661	probable transpos
452	52.5	11.4	296	2	S09261	probable transpos	525	52	11.3	297	2	T47857	myb protein-like -
453	52.5	11.4	301	2	B64189	glycine cleavage s	526	52	11.3	310	2	S46239	ribosome-inactivat
454	52.5	11.4	309	2	A87564	membrane protein,	527	52	11.3	310	2	T32006	hypothetical prote
455	52.5	11.4	310	2	C39778	tagatose-6-phospha	528	52	11.3	320	2	A12305	hypothetical prote
456	52.5	11.4	310	2	T31125	hypothetical prote	529	52	11.3	327	2	AH2608	transcription regu
457	52.5	11.4	322	2	AF1031	hypothetical prote	530	52	11.3	327	2	G97390	arac family trans
458	52.5	11.4	332	2	C72310	conserved hypotnet	531	52	11.3	359	2	A43532	B-cell surface ant
459	52.5	11.4	334	2	D81217	hypothetical prote	532	52	11.3	364	2	B71139	hypothetical prote
460	52.5	11.4	334	2	T33950	hypothetical prote	533	52	11.3	372	2	B64819	probable membrane
461	52.5	11.4	342	2	C48455	cysteine proteinas	534	52	11.3	372	2	B85591	hypothetical prote
462	52.5	11.4	356	2	D84280	hypothetical prote	535	52	11.3	372	2	G90740	hypothetical prote
463	52.5	11.4	360	2	T51344	RNA helicase RH18	536	52	11.3	375	2	S47704	hypothetical 41.1K
464	52.5	11.4	366	2	A49877	prostaglandin F re	537	52	11.3	375	2	F91173	probable transpor
465	52.5	11.4	377	2	C69758	amino acid transpo	538	52	11.3	379	2	F86019	hypothetical prote
466	52.5	11.4	394	2	B86507	hypothetical prote	539	52	11.3	397	2	F83152	conserved hypotnet
467	52.5	11.4	394	2	B81554	hypothetical prote	540	52	11.3	397	2	B70048	conserved hypotnet

541	52	11.3	417	2	B69804	multitdug resistan	614	51.5	11.2	410	2	S45894	regulatory protein
542	52	11.3	457	2	S39079	puff C-8 protein -	615	51.5	11.2	429	2	F87038	probable membrane
543	52	11.3	469	2	D81017	chloride channel p	616	51.5	11.2	438	2	A83037	probable MFS trans
544	52	11.3	470	2	C70641	hypothetical prote	617	51.5	11.2	450	2	C96704	unknown protein, 2
545	52	11.3	491	2	S75449	hypothetical prote	618	51.5	11.2	451	2	F75177	tryptophan synthas
546	52	11.3	502	2	G87433	conserved hypotet	619	51.5	11.2	474	1	A40570	lipoprotein lipase
547	52	11.3	502	2	T29729	hypothetical prote	620	51.5	11.2	478	1	C42790	cystathionine beta
548	52	11.3	526	2	H85891	hydrogenase 4 memb	621	51.5	11.2	478	1	C30763	hypothetical prote
549	52	11.3	526	2	D91047	hydrogenase 4 memb	622	51.5	11.2	478	2	T32476	probable protein-t
550	52	11.3	530	2	D87255	apolipoprotein N-a	623	51.5	11.2	481	2	B82130	pyruvate kinase II
551	52	11.3	534	2	T27054	hypothetical prote	624	51.5	11.2	493	2	T21445	hypothetical prote
552	52	11.3	544	2	T17422	halogenase-like pr	625	51.5	11.2	509	2	G82409	glyceroldehyde 3-p
553	52	11.3	548	2	C82698	electron transfer	626	51.5	11.2	513	2	T34546	hypothetical prote
554	52	11.3	553	2	S75892	probable glycerol-	627	51.5	11.2	525	2	A70735	probable gua prot
555	52	11.3	567	2	H87370	major facilitator	628	51.5	11.2	531	2	D96965	PTS system, arbuti
556	52	11.3	573	2	A33533	cell surface glyco	629	51.5	11.2	534	1	JU00274	cell fusion glycop
557	52	11.3	579	2	A64100	inner membrane cop	630	51.5	11.2	536	2	D81700	CTP synthase TC045
558	52	11.3	635	2	H65626	PTS fructose-speci	631	51.5	11.2	536	2	F85697	hypothetical prote
559	52	11.3	706	2	H81943	probable polyribon	632	51.5	11.2	536	2	D64865	probable Na+/H+-ex
560	52	11.3	707	2	C81161	polyribonucleotide	633	51.5	11.2	536	2	P90839	hypothetical prote
561	52	11.3	733	2	F82965	hypothetical prote	634	51.5	11.2	540	1	JU0470	site-specific DNA-
562	52	11.3	738	2	S37876	glutamine-rich pro	635	51.5	11.2	541	1	A70022	multitdug-efflux t
563	52	11.3	773	2	AH2061	hypothetical prote	636	51.5	11.2	541	2	UN0511	heat shock protein
564	52	11.3	823	2	A96737	hypothetical prote	637	51.5	11.2	547	2	T46059	MAP kinase - Arabi
565	52	11.3	840	2	T21333	hypothetical prote	638	51.5	11.2	549	2	T51099	MAP kinase [impor
566	52	11.3	869	2	A95156	hypothetical prote	639	51.5	11.2	550	1	E48556	cell fusion glycop
567	52	11.3	878	2	D98022	conserved hypotet	640	51.5	11.2	558	2	C72391	conserved hypotet
568	52	11.3	906	2	A82533	hypothetical prote	641	51.5	11.2	560	2	S27387	interferon alpha x
569	52	11.3	1016	2	T00375	hypothetical prote	642	51.5	11.2	561	1	A42790	cycatichionine beta
570	52	11.3	1017	2	T37201	hypothetical prote	643	51.5	11.2	623	2	T35377	probable membrane
571	52	11.3	1106	2	A97647	cation efflux synt	644	51.5	11.2	666	2	AF0861	transketolase (EC
572	52	11.3	1106	2	AC2870	Acr family transpo	645	51.5	11.2	667	1	A48660	transketolase (EC
573	52	11.3	1146	2	T09112	probable sensor ki	646	51.5	11.2	667	2	G91044	transketolase 2 is
574	52	11.3	1146	2	A82174	senary box sensor	647	51.5	11.2	667	2	B85889	transketolase 2 is
575	52	11.3	1484	2	C97196	probable membrane	648	51.5	11.2	682	2	T12715	NAHD2 dehydrogenas
576	52	11.3	1484	2	S68453	sodium channel pro	649	51.5	11.2	724	2	T19601	hypothetical prote
577	52	11.3	1939	2	A44467	voltage-dependent	650	51.5	11.2	726	2	T31287	hypothetical prote
578	52	11.3	2220	2	A45290	calcium channel pr	651	51.5	11.2	763	2	A13443	Na+/H+ antiporter
579	52	11.3	3429	2	T13853	hypothetical prote	652	51.5	11.2	765	2	B75288	hypothetical prote
580	51.5	11.2	116	2	A83693	transcription regu	653	51.5	11.2	795	2	A80705	phenylalanyl-tRNA
581	51.5	11.2	122	1	PSABA	phospholipase A2 (654	51.5	11.2	829	2	T29372	hypothetical prote
582	51.5	11.2	131	2	C72563	hypothetical prote	655	51.5	11.2	846	2	T27282	hypothetical prote
583	51.5	11.2	146	2	S42570	flavodoxin - Desul	656	51.5	11.2	869	2	C56617	cifac protein precu
584	51.5	11.2	167	2	H86784	VP829-like phospho	657	51.5	11.2	1451	1	J01719	E2 glycoprotein pr
585	51.5	11.2	172	2	F75491	conserved hypotet	658	51.5	11.2	1755	2	T51532	hypothetical prote
586	51.5	11.2	206	1	I40173	orotate phosphorib	659	51.5	11.2	1784	2	T43167	sodium channel pro
587	51.5	11.2	209	2	T00733	hypothetical prote	660	51.5	11.2	2301	1	GNNYTN	genome polyprotein
588	51.5	11.2	212	1	A49436	dual specificity p	661	51.5	11.2	2303	1	GNNYTM	genome polyprotein
589	51.5	11.2	222	2	H64495	cobalamin bioynth	662	51.5	11.2	89	2	AH3403	hypothetical prote
590	51.5	11.2	270	2	A29934	pancreatic elastas	663	51.5	11.1	93	2	A86491	conserved hypotet
591	51.5	11.2	276	2	A70425	hypothetical prote	664	51.5	11.1	93	2	F72130	hypothetical prote
592	51.5	11.2	282	2	AC2294	hypothetical prote	665	51.5	11.1	95	2	AG2439	hypothetical prote
593	51.5	11.2	289	2	G97192	oligopeptide ABC-t	666	51.5	11.1	106	2	C75415	hypothetical prote
594	51.5	11.2	299	2	B95939	probable spermidin	667	51.5	11.1	152	2	A72588	conserved hypotet
595	51.5	11.2	299	2	H97884	hypothetical prote	668	51.5	11.1	152	2	H95153	hypothetical prote
596	51.5	11.2	312	2	B69170	UDP-N-acetylmuram	669	51.5	11.1	173	2	AF2518	hypothetical prote
597	51.5	11.2	313	2	S75329	hypothetical prote	670	51.5	11.1	188	2	T15651	multiple antibioci
598	51.5	11.2	314	2	T21971	hypothetical prote	671	51.5	11.1	201	2	B75039	probable orotate p
599	51.5	11.2	319	2	T02691	gloeyvi protein g1	672	51.5	11.1	202	2	A81441	conserved hypotet
600	51.5	11.2	342	2	T16806	hypothetical prote	673	51.5	11.1	204	2	A82389	cysteine proteins
601	51.5	11.2	355	2	S76667	hypothetical prote	674	51.5	11.1	212	2	I67437	hypothetical prote
602	51.5	11.2	364	2	G82734	acetylmurithine de	675	51.5	11.1	221	2	S75146	hypothetical prote
603	51.5	11.2	366	2	I53488	prostaalandin F2 a	676	51.5	11.1	229	2	B85806	hypothetical prote
604	51.5	11.2	366	2	S51281	F2-alpha receptor	677	51.5	11.1	229	2	D90958	hypothetical prote
605	51.5	11.2	370	2	AH1485	fructose-specific	678	51.5	11.1	240	2	T02059	hypothetical prote
606	51.5	11.2	370	2	AH1124	peptide ABC transp	679	51.5	11.1	246	2	T28166	histone H1 - maize
607	51.5	11.2	376	2	A75381	probable acetylpol	680	51.5	11.1	246	2	A71192	probable glucose 1
608	51.5	11.2	380	2	D83174	G protein-coupled	681	51.5	11.1	261	2	AC2280	glutathione S-tran
609	51.5	11.2	381	2	A35300	amino transferase,	682	51.5	11.1	263	2	G96978	uncharacterized co
610	51.5	11.2	381	2	F87553	ompF-like porin 11	683	51.5	11.1	264	2	C96978	phosphatidate cycl
611	51.5	11.2	382	2	G84971	Edg-1 orphan recep	684	51.5	11.1	265	2	B81229	embryonic abundant
612	51.5	11.2	383	2	I53870	hypothetical prote	685	51.5	11.1	265	2	A82000	
613	51.5	11.2	390	2	C95954		686	51.5	11.1	268	2	S03328	

687	51	11.1	279	2	T22051	hypothetical prote	760	50.5	11.0	173	2	SS9864	TRAP-like protein
688	51	11.1	282	2	E64063	hypothetical prote	761	50.5	11.0	201	1	IMBPSB	immunity protein -
689	51	11.1	282	2	A41025	aspergillopepsin I	762	50.5	11.0	204	2	E83036	hypothetical prote
690	51	11.1	285	2	T15498	hypothetical prote	763	50.5	11.0	208	2	F71314	probable transcrip
691	51	11.1	295	2	F90938	hypothetical prote	764	50.5	11.0	217	2	T51062	MHC class II beta
692	51	11.1	295	2	B85664	transposase for IS	765	50.5	11.0	224	2	T34686	probable integral
693	51	11.1	295	2	D90801	hypothetical prote	766	50.5	11.0	227	2	T12797	immunity protein d
694	51	11.1	295	2	B85613	probable transpos	767	50.5	11.0	228	2	C28551	hypothetical prote
695	51	11.1	309	2	AF0746	mobility protein B	768	50.5	11.0	231	2	H81698	hypothetical prote
696	51	11.1	321	2	A55090	cathepsin O (EC 3.	769	50.5	11.0	233	2	JH0372	42k surface glycop
697	51	11.1	328	1	S64306	hypothetical prote	770	50.5	11.0	234	2	E95360	hypothetical prote
698	51	11.1	328	1	AG0645	spermidine/putresc	771	50.5	11.0	240	1	TQEC34	transposase - Bsch
699	51	11.1	355	2	B26785	protein F10A5.28 (772	50.5	11.0	247	2	T51060	MHC class II beta
700	51	11.1	357	2	A71523	probable chorismat	773	50.5	11.0	247	2	T51059	MHC class II beta
701	51	11.1	361	2	A45211	prostaglandin E re	774	50.5	11.0	249	2	S75671	hypothetical prote
702	51	11.1	362	2	A53058	prostaglandin F2-a	775	50.5	11.0	249	2	H95256	ABC transporter, p
703	51	11.1	364	2	S65009	prostaglandin E re	776	50.5	11.0	250	2	T09160	proteasome subunit
704	51	11.1	365	2	A42414	prostaglandin E re	777	50.5	11.0	252	2	F70711	probable membran
705	51	11.1	372	2	S75587	H+/Ca2+ exchanging	778	50.5	11.0	253	2	A98122	hypothetical prote
706	51	11.1	375	2	T03256	GTP-binding protei	779	50.5	11.0	255	2	JN0829	3alpha-hydroxyster
707	51	11.1	377	2	T04086	GTP-binding protei	780	50.5	11.0	258	2	A69805	hypothetical prote
708	51	11.1	377	2	T16985	GRP-binding protei	781	50.5	11.0	260	2	F82954	probable short-cha
709	51	11.1	379	2	AB2423	hypothetical prote	782	50.5	11.0	264	2	D87504	hypothetical prote
710	51	11.1	384	2	AE9622	ferrichrome ABC tr	783	50.5	11.0	286	2	E86844	shikimate 5-dehydr
711	51	11.1	394	2	B85535	probable transport	784	50.5	11.0	288	2	F85818	hypothetical prote
712	51	11.1	394	2	F90684	probable transport	785	50.5	11.0	293	2	A83623	hypothetical prote
713	51	11.1	402	2	B82491	MupC family protei	786	50.5	11.0	296	2	A85841	probable transpos
714	51	11.1	404	2	T39270	conserved hypotet	787	50.5	11.0	296	2	D91284	hypothetical prote
715	51	11.1	409	2	G90491	conserved hypotet	788	50.5	11.0	296	2	F90868	hypothetical prote
716	51	11.1	416	2	T14554	calreticulin - bee	789	50.5	11.0	296	2	D90955	hypothetical prote
717	51	11.1	418	2	S31124	hypothetical prote	790	50.5	11.0	296	2	E91020	hypothetical prote
718	51	11.1	421	2	B82062	conserved hypotet	791	50.5	11.0	296	2	F91132	hypothetical prote
719	51	11.1	423	2	AB0054	probable Na+ depen	792	50.5	11.0	296	2	F91111	hypothetical prote
720	51	11.1	435	2	E71350	probable aspartate	793	50.5	11.0	296	2	G90998	hypothetical prote
721	51	11.1	439	2	S58327	cobalt accumulat	794	50.5	11.0	296	2	T00240	transposase - Bsch
722	51	11.1	439	2	T18898	hypothetical prote	795	50.5	11.0	296	2	B90837	hypothetical prote
723	51	11.1	440	2	AD1073	thymidine phosphor	796	50.5	11.0	296	2	C91065	hypothetical prote
724	51	11.1	449	2	C86496	hypothetical prote	797	50.5	11.0	296	2	H90779	hypothetical prote
725	51	11.1	449	2	D72127	hypothetical prote	798	50.5	11.0	296	2	C90906	hypothetical prote
726	51	11.1	449	2	AB1544	hypothetical prote	799	50.5	11.0	296	2	A99972	hypothetical prote
727	51	11.1	450	2	AB1420	PTS cellulobiose-spe	800	50.5	11.0	297	2	T09542	endonuclease G (EC
728	51	11.1	450	2	ACT195	PTS cellulobiose-spe	801	50.5	11.0	297	2	T45436	hypothetical membr
729	51	11.1	458	1	YTB316	tetracycline resis	802	50.5	11.0	302	2	S02728	actindain (EC 3.4
730	51	11.1	460	2	S06469	photoystem II chl	803	50.5	11.0	302	2	S60955	probable membrane
731	51	11.1	466	2	E84132	aminopeptidase B3	804	50.5	11.0	313	2	AH1300	malonyl CoA-acyl c
732	51	11.1	468	2	AE9468	ammonium transport	805	50.5	11.0	314	2	F86928	34 kDa antigen (im
733	51	11.1	485	2	A72006	arginine/ornithine	806	50.5	11.0	317	2	T27994	hypothetical prote
734	51	11.1	514	2	A86671	Ammonium transport	807	50.5	11.0	324	2	A86839	conserved hypotet
735	51	11.1	516	2	T09859	cytochrome-c oxida	808	50.5	11.0	327	2	S61962	probable membrane
736	51	11.1	525	2	T00459	hypothetical prote	809	50.5	11.0	332	2	S77386	nitratre transport
737	51	11.1	528	2	T22583	hypothetical prote	810	50.5	11.0	346	2	C71390	NMDH2 dehydrogen
738	51	11.1	531	2	T12406	cytochrome-c oxida	811	50.5	11.0	351	2	A69808	UDP-N-acetylglucos
739	51	11.1	560	2	T51485	sugar transporter-	812	50.5	11.0	355	1	BVECMG	hypothetical prote
740	51	11.1	616	2	T07611	aconitate hydrat	813	50.5	11.0	355	2	F85491	hypothetical prote
741	51	11.1	635	1	AE4162	cytochrome c-type	814	50.5	11.0	355	2	F90640	hypothetical prote
742	51	11.1	639	2	J00607	glucan 1,4-alpha-g	815	50.5	11.0	361	2	F87286	cation efflux fami
743	51	11.1	659	2	AE6802	unknown protein [i	816	50.5	11.0	362	2	JC7559	ephingosine 1-phos
744	51	11.1	745	1	A70458	phosphoribosylform	817	50.5	11.0	364	2	H70776	hypothetical prote
745	51	11.1	754	1	A39329	phospholipase A2 (818	50.5	11.0	379	2	B51044	geranylgeranyl-dip
746	51	11.1	754	1	S37403	transcription fact	819	50.5	11.0	379	2	T45768	protein phosphat
747	51	11.1	770	2	T50308	probable translati	820	50.5	11.0	382	2	H90500	glycolate oxidase
748	51	11.1	778	2	E97224	ATP-dependent Lon	821	50.5	11.0	398	2	S75202	hypothetical prote
749	51	11.1	854	2	T23837	hypothetical prote	822	50.5	11.0	399	2	T26257	hypothetical prote
750	51	11.1	862	2	T46289	hypothetical prote	823	50.5	11.0	406	2	T27947	hypothetical prote
751	51	11.1	862	2	T16282	hypothetical prote	824	50.5	11.0	407	2	E70309	hypothetical prote
752	51	11.1	887	2	T01113	translacton initia	825	50.5	11.0	408	2	T29949	hypothetical prote
753	51	11.1	967	2	A30325	membrane alanyl am	826	50.5	11.0	410	2	UC7584	basic helix-loop-h
754	51	11.1	1075	2	D70568	hypothetical prote	827	50.5	11.0	411	2	AG3003	conserved hypotet
755	51	11.1	1325	2	A64905	yakK protein - Bsc	828	50.5	11.0	411	2	B98280	hypothetical prote
756	51	11.1	1790	1	S27772	vitellogenin precu	829	50.5	11.0	421	2	D70868	probable liipo prot
757	51	11.0	137	2	D75337	hypothetical prote	830	50.5	11.0	424	2	A71846	glycinamide ribonu
758	50.5	11.0	141	2	E72580	hypothetical prote	831	50.5	11.0	424	2	B64672	probable chloride
759	50.5	11.0	155	2	T22027	hypothetical prote	832	50.5	11.0	441	2	AF0411	

833	50.5	11.0	442	2	S56057	heavy metal ion re	906	50	10.8	214	2	T10737	extensin-like cell
834	50.5	11.0	448	2	A83775	hypothetical prote	907	50	10.8	219	2	A11441	hypothetical prote
835	50.5	11.0	460	2	G85525	probable deaminase	908	50	10.8	216	2	T38019	uracil phosphoribo
836	50.5	11.0	460	2	E90675	probable deaminase	909	50	10.8	232	2	S29001	G protein-coupled
837	50.5	11.0	470	2	T20851	hypothetical prote	910	50	10.8	236	2	T32473	hypothetical prote
838	50.5	11.0	471	2	D83546	probable amino aci	911	50	10.8	238	2	B64509	hypothetical prote
839	50.5	11.0	474	1	JH0790	lipoprotein lipase	912	50	10.8	250	2	S51206	cruxinodopsin-1 -
840	50.5	11.0	507	2	T27627	hypothetical prote	913	50	10.8	255	2	A71351	probable cobalt AB
841	50.5	11.0	509	2	G81929	probable iron-purc	914	50	10.8	256	2	A81277	probable oxidoredu
842	50.5	11.0	510	2	T20850	hypothetical prote	915	50	10.8	259	2	C75151	oxidoreductase PAB
843	50.5	11.0	515	2	G75267	ABC transporter, p	916	50	10.8	265	2	D81315	hypothetical prote
844	50.5	11.0	517	2	S21042	cytochrome-c oxida	917	50	10.8	265	2	G97460	hypothetical prote
845	50.5	11.0	518	2	S34565	gene G protein - h	918	50	10.8	268	2	C83369	probable binding p
846	50.5	11.0	518	2	F70831	probable PPE prote	919	50	10.8	274	2	E75614	conserved hypothet
847	50.5	11.0	520	2	AD2383	Na+/H+-exchanging	920	50	10.8	293	2	T36063	probable integral
848	50.5	11.0	526	2	G83436	hypothetical prote	921	50	10.8	295	2	B85787	probable transpos
849	50.5	11.0	529	1	YRHU1	monophenol monoox	922	50	10.8	295	2	T00315	transposase - Esch
850	50.5	11.0	543	2	T37570	WD repeat protein	923	50	10.8	296	2	167971	transposase - Esch
851	50.5	11.0	543	2	S65462	glucose transport	924	50	10.8	296	2	D90398	conserved hypothet
852	50.5	11.0	544	2	AD1979	permease protein o	925	50	10.8	299	2	S50803	hypothetical prote
853	50.5	11.0	545	2	AC1914	sterol carrier pro	926	50	10.8	304	2	A72596	hypothetical prote
854	50.5	11.0	546	2	B40407	mandelonitrile lya	927	50	10.8	308	2	S22928	ubiquinol-cytocho
855	50.5	11.0	563	2	S32156	probable nitratre t	928	50	10.8	314	2	S72525	pectinesterase (EC
856	50.5	11.0	577	2	T52608	hypothetical prote	929	50	10.8	317	2	B87666	homoserine kinase
857	50.5	11.0	584	2	S40013	hypothetical prote	930	50	10.8	332	2	C87426	cysteine synthase
858	50.5	11.0	586	2	F84663	probable nitratre t	931	50	10.8	332	2	C84061	ferrichrome ABC tr
859	50.5	11.0	595	2	AD2718	aspartyl -tRNA synt	932	50	10.8	333	2	T36036	probable integral
860	50.5	11.0	595	2	D97500	aspartyl -tRNA syn	933	50	10.8	337	2	AG0802	probable semialdeh
861	50.5	11.0	608	2	S76192	hypothetical prote	934	50	10.8	341	2	D48435	cysteine proteinas
862	50.5	11.0	684	2	T25603	hypothetical prote	935	50	10.8	348	2	B86818	dehydrogenase (imp
863	50.5	11.0	688	2	H96681	protein F1E22.10 (936	50	10.8	357	2	D83685	nicotinate-nucleot
864	50.5	11.0	704	2	F87706	proyl oligopeptid	937	50	10.8	357	2	T09321	JUN kinase-activat
865	50.5	11.0	712	2	AD2721	H+ translocating p	938	50	10.8	372	2	S20056	para-hydroxybenzo
866	50.5	11.0	714	2	H97502	h+ translocating p	939	50	10.8	375	2	T25089	hypothetical prote
867	50.5	11.0	731	2	E82922	phosphate transpor	940	50	10.8	380	2	A71390	ubiquinol-cytocho
868	50.5	11.0	736	2	AC2821	bacteriophytochrom	941	50	10.8	388	2	D69468	ammonium transport
869	50.5	11.0	745	2	C97599	cyanobacterial phy	942	50	10.8	388	2	AF0183	probable exported
870	50.5	11.0	819	2	F87708	cell division prot	943	50	10.8	393	2	S61659	KRPA protein - yea
871	50.5	11.0	827	2	A95877	hypothetical prote	944	50	10.8	397	2	E91296	probable thymidine
872	50.5	11.0	908	2	A10327	two-component regu	945	50	10.8	407	2	F70318	hypothetical prote
873	50.5	11.0	942	1	U01674	protein kinase TWK	946	50	10.8	407	2	G75268	hypothetical prote
874	50.5	11.0	962	2	T05845	hypothetical prote	947	50	10.8	414	1	E70708	cytochrome P450 RV
875	50.5	11.0	1163	1	RMHU1C	cell surface glyco	948	50	10.8	420	2	A82856	conserved hypothet
876	50.5	11.0	1188	2	T20333	hypothetical prote	949	50	10.8	430	2	A12379	hypothetical prote
877	50.5	11.0	1265	2	T47626	structural mainten	950	50	10.8	435	2	G86907	D-alanyl-D-alanine
878	50.5	11.0	1317	2	T03748	apoptosis associat	951	50	10.8	440	1	S36606	thymidine phosphor
879	50.5	11.0	1345	2	T44204	major capsid prote	952	50	10.8	440	2	G86137	Na+-transporting A
880	50.5	11.0	1345	2	T44017	hypothetical prote	953	50	10.8	449	2	H69862	chromogranin A pre
881	50.5	11.0	1400	2	B70963	hypothetical prote	954	50	10.8	457	1	A28468	streptogristin C (E
882	50.5	11.0	1447	1	VGJHE3	E2 glycoprotein pr	955	50	10.8	457	2	U0145	interleukin-6 rece
883	50.5	11.0	1449	1	VGJHE2	E2 glycoprotein pr	956	50	10.8	460	2	U0145	photosystem II chl
884	50.5	11.0	1449	1	A43573	E2 glycoprotein pr	957	50	10.8	473	1	F2R244	photosystem II chl
885	50.5	11.0	1449	1	VGJHFS	E2 glycoprotein pr	958	50	10.8	473	1	F2SP44	photosystem II chl
886	50.5	11.0	1577	2	T15851	hypothetical prote	959	50	10.8	473	2	T08998	photosystem II pro
887	50.5	11.0	1672	2	C81675	polymorphic membra	960	50	10.8	476	2	AC2306	hypothetical prote
888	50.5	11.0	1921	2	T13827	kinesin-73 - fruit	961	50	10.8	489	2	A11639	multidrug-efflux t
889	50	10.8	89	2	H83795	hypothetical prote	962	50	10.8	494	2	C70940	probable cobq prot
890	50	10.8	100	2	A12298	cobalt transport p	963	50	10.8	514	2	F98149	hypothetical prote
891	50	10.8	102	2	A75417	hypothetical prote	964	50	10.8	514	2	C49507	potassium channel
892	50	10.8	121	2	B72546	hypothetical prote	965	50	10.8	516	2	S39686	Na+-dependent sym
893	50	10.8	138	2	JC1342	phospholipase A2 (966	50	10.8	532	2	JC1392	monophenol monoox
894	50	10.8	147	2	S70109	hypothetical prote	967	50	10.8	533	2	AE3138	hypothetical prote
895	50	10.8	150	2	G72660	hypothetical prote	968	50	10.8	538	2	C83284	probable biotin-de
896	50	10.8	170	2	B86842	hypothetical prote	969	50	10.8	538	2	C86976	ppe-family protein
897	50	10.8	175	2	AE1149	NADH2 dehydrogenas	970	50	10.8	539	2	C83758	cephalosporin acyl
898	50	10.8	175	2	AE1149	hypothetical prote	971	50	10.8	542	2	S50361	probable membrane
899	50	10.8	186	2	E82625	outer membrane pro	972	50	10.8	545	2	T18694	hypothetical prote
900	50	10.8	195	2	T39603	BAG-family molecul	973	50	10.8	545	2	T39499	conserved hypothet
901	50	10.8	203	2	D81934	probable periplasm	974	50	10.8	573	2	D83440	probable sulfate t
902	50	10.8	203	2	F81171	cyclic protein NM	975	50	10.8	588	2	T25248	hypothetical prote
903	50	10.8	211	2	A47686	bacteriorhodopsin-	976	50	10.8	598	2	S66669	potassium channel
904	50	10.8	211	2	AC0268	probable exported	977	50	10.8	602	2	A49507	potassium channel
905	50	10.8	213	2	G75521	ABC transporter, A	978	50	10.8	602	2	JH0166	potassium voltage-

979	50	10.8	606	2	S57552	hypothetical prote	1052	49.5	10.7	400	2	T46383	hypothetical prote
980	50	10.8	613	2	A56031	potassium channel	1053	49.5	10.7	401	2	D83022	hypothetical prote
981	50	10.8	614	2	E86194	hypothetical prote	1054	49.5	10.7	403	2	T09332	DNA polymerase pro
982	50	10.8	700	2	B81266	DNA topoisomerase	1055	49.5	10.7	424	2	D75530	probable beta-lact
983	50	10.8	749	1	B39898	phospholipase A2 (1056	49.5	10.7	427	2	A49518	kallicreasin precu
984	50	10.8	756	2	C84682	hypothetical prote	1057	49.5	10.7	430	1	S32570	mALC protein - Str
985	50	10.8	789	2	A82688	Na/H+ antiporter	1058	49.5	10.7	430	2	AF1356	hypothetical prote
986	50	10.8	789	2	H97469	probable NADH dehy	1059	49.5	10.7	430	2	AG1726	hypothetical prote
987	50	10.8	810	1	P2M88B	2a protein - broad	1060	49.5	10.7	432	2	H64383	Na+ transporter -
988	50	10.8	828	1	JC5807	trp3 protein - rat	1061	49.5	10.7	443	2	AE0309	probable sugar tra
989	50	10.8	836	2	F70363	cation transportin	1062	49.5	10.7	469	2	T34645	hypothetical prote
990	50	10.8	836	2	C97525	clpA protein (A122	1063	49.5	10.7	469	2	S74825	probable Rieseke ir
991	50	10.8	836	2	AD2744	ATP-dependent Clp	1064	49.5	10.7	476	1	VMUT4R	variant surface gl
992	50	10.8	876	2	T07101	lipoxigenase (EC 1	1065	49.5	10.7	476	2	B86829	multidrug transpor
993	50	10.8	933	2	F97717	hypothetical prote	1066	49.5	10.7	478	2	T33942	hypothetical prote
994	50	10.8	1015	2	T15830	hypothetical prote	1067	49.5	10.7	502	2	T26256	hypothetical prote
995	50	10.8	1021	2	A86421	Receptor-like seri	1068	49.5	10.7	505	2	G90419	metabolic permeas
996	50	10.8	1022	2	F87635	AcetB/AcrD/AcrF fam	1069	49.5	10.7	508	2	H86474	hypothetical prote
997	50	10.8	1277	2	T14152	synaptic scaffoldi	1070	49.5	10.7	514	2	F87592	hypothetical prote
998	50	10.8	1338	2	T40993	protein kinase cek	1071	49.5	10.7	524	2	F85429	actin interacting
999	50	10.8	1381	2	T31083	paranodin - rat	1072	49.5	10.7	538	2	T40298	membrane transport
1000	50	10.8	1479	2	T42710	mannose receptor,	1073	49.5	10.7	538	2	A83018	probable sodium/hy
1001	50	10.8	1498	2	B97355	DNA segregation AT	1074	49.5	10.7	552	2	A51027	L-ascorbate oxidas
1002	50	10.8	1505	2	S26765	genome polyprotein	1075	49.5	10.7	553	2	B90153	2-isopropylmalate
1003	50	10.8	1524	2	S68553	surface layer prot	1076	49.5	10.7	556	2	T46892	K+-transporting AT
1004	50	10.8	1526	2	A86528	protein F27015.14	1077	49.5	10.7	557	2	H97351	K+-transporting AT
1005	50	10.8	1687	2	S41742	calcium channel al	1078	49.5	10.7	559	2	C87307	hypothetical prote
1006	50	10.8	2109	2	T31352	hypothetical prote	1079	49.5	10.7	566	2	B82173	probable ABC trans
1007	50	10.8	2819	2	A90551	conserved hypother	1080	49.5	10.7	579	2	S11027	L-ascorbate oxidas
1008	49.5	10.7	63	2	B90031	hypothetical prote	1081	49.5	10.7	583	2	T48473	amino acid transpo
1009	49.5	10.7	119	2	AD2901	Ig H chain v regio	1082	49.5	10.7	583	2	E83794	ABC transporter (A
1010	49.5	10.7	130	2	AD2901	hypothetical prote	1083	49.5	10.7	586	1	E69314	replication licens
1011	49.5	10.7	130	2	S67024	probable membrane	1084	49.5	10.7	660	2	B97853	NMDH2 dehydrogenas
1012	49.5	10.7	150	2	F87507	conserved hypother	1085	49.5	10.7	686	2	E71895	NMDH2 dehydrogenas
1013	49.5	10.7	160	2	C35542	riboseomal protei	1086	49.5	10.7	697	2	T13670	NMDH2 dehydrogenas
1014	49.5	10.7	165	2	F97676	succinate dehydrog	1087	49.5	10.7	698	2	T12625	NMDH2 dehydrogenas
1015	49.5	10.7	165	2	S50195	oleosin - rape	1088	49.5	10.7	699	2	T12673	NMDH2 dehydrogenas
1016	49.5	10.7	171	2	S22194	hypothetical prote	1089	49.5	10.7	700	2	T23629	hypothetical prote
1017	49.5	10.7	172	2	I39644	apric protein - Ac	1090	49.5	10.7	701	2	T13056	NMDH2 dehydrogenas
1018	49.5	10.7	197	2	A82056	hypothetical prote	1091	49.5	10.7	702	2	T13587	NMDH2 dehydrogenas
1019	49.5	10.7	214	2	D83881	siderophore (surfa	1092	49.5	10.7	702	2	T13058	NMDH2 dehydrogenas
1020	49.5	10.7	218	2	AC1253	glycine betaine/ca	1093	49.5	10.7	702	2	T12624	NMDH2 dehydrogenas
1021	49.5	10.7	218	2	AT1615	cell division prot	1094	49.5	10.7	702	2	T13469	NMDH2 dehydrogenas
1022	49.5	10.7	226	2	F87449	glycine betaine/ca	1095	49.5	10.7	703	2	T13074	NMDH2 dehydrogenas
1023	49.5	10.7	244	2	A84885	hypothetical prote	1096	49.5	10.7	703	2	T13696	NMDH2 dehydrogenas
1024	49.5	10.7	251	2	AF2281	hypothetical prote	1097	49.5	10.7	706	2	T12748	NMDH2 dehydrogenas
1025	49.5	10.7	252	1	A34702	hypothetical prote	1098	49.5	10.7	721	2	F82198	probable toxin sec
1026	49.5	10.7	255	2	H81302	amphiregulin precu	1099	49.5	10.7	732	2	A83481	probable TonB-depe
1027	49.5	10.7	275	2	H90251	maltose transport	1100	49.5	10.7	734	1	DER2N5	NMDH2 dehydrogenas
1028	49.5	10.7	294	2	B83040	ribosomal protein	1101	49.5	10.7	738	2	S58612	NMDH2 dehydrogenas
1029	49.5	10.7	295	2	T04483	probable ring fing	1102	49.5	10.7	740	2	B84741	NMDH2 dehydrogenas
1030	49.5	10.7	301	1	S10456	cytochrome c-type	1103	49.5	10.7	745	2	B84673	hypothetical prote
1031	49.5	10.7	302	1	S10456	hypothetical prote	1104	49.5	10.7	753	2	F69338	pyruvate, water di
1032	49.5	10.7	305	2	AT0847	Iron transport pro	1105	49.5	10.7	770	2	S56695	transducin-like en
1033	49.5	10.7	313	2	AH1672	malonyl CoA-acyl c	1106	49.5	10.7	776	2	S45495	hypothetical yong
1034	49.5	10.7	315	2	B98226	hypothetical prote	1107	49.5	10.7	788	1	I59282	diacylglycerol kin
1035	49.5	10.7	315	2	AF3060	conserved hypother	1108	49.5	10.7	795	2	D82225	phenylalaninyl-tRNA
1036	49.5	10.7	327	2	T32164	hypothetical prote	1109	49.5	10.7	822	2	T25866	hypothetical prote
1037	49.5	10.7	328	2	AD1916	alcohol dehydrogen	1110	49.5	10.7	826	2	AC0086	outer membrane ush
1038	49.5	10.7	330	2	H75353	probable noex prot	1111	49.5	10.7	850	2	JC5700	ExbB kinase activa
1039	49.5	10.7	332	2	T33799	hypothetical prote	1112	49.5	10.7	875	2	T12794	hypothetical yong
1040	49.5	10.7	334	2	T23444	hypothetical prote	1113	49.5	10.7	888	2	A54280	cell differentiat
1041	49.5	10.7	341	2	C96304	probable oligopept	1114	49.5	10.7	914	1	JN0550	iodide peroxidase
1042	49.5	10.7	341	2	AB82979	hypothetical prote	1115	49.5	10.7	945	2	S77052	cation-transportin
1043	49.5	10.7	348	2	B48435	cysteine proteinas	1116	49.5	10.7	1039	2	T38447	tetratricopeptide
1044	49.5	10.7	360	2	B87286	conserved hypother	1117	49.5	10.7	1069	2	D85383	hypothetical prote
1045	49.5	10.7	367	2	C68500	group II decarboxy	1118	49.5	10.7	1084	2	T15616	hypothetical prote
1046	49.5	10.7	368	1	Q0B5HG	early nuclear anti	1119	49.5	10.7	1121	2	UC7329	WD-repeat protein
1047	49.5	10.7	372	1	D69442	conserved hypother	1120	49.5	10.7	1132	2	T31107	telomerase reverse
1048	49.5	10.7	374	1	I39857	spore germination	1121	49.5	10.7	1163	2	A56097	arylporin-binding
1049	49.5	10.7	374	2	T21513	hypothetical prote	1122	49.5	10.7	1195	2	S76592	5-methyltetrahydro
1050	49.5	10.7	380	1	TAGB	actindinain (BC 3.4	1123	49.5	10.7	1354	2	AG0538	Rna-family protein
1051	49.5	10.7	391	2	T43987	ppa1, pol processi	1124	49.5	10.7	1461	2	E90696	hypothetical prote

1125	49.5	10.7	1461	2	A85547	hypothetical prote	1198	49	10.6	355	2	S41686	geranylgeranyltran
1126	49.5	10.7	1492	2	A39322	cyclic fibroblasts tr	1199	49	10.6	366	2	A64950	membrane-bound pen
1127	49.5	10.7	2150	2	T08165	RNA1 polypeptide	1200	49	10.6	366	2	C58800	probable cytochrom
1128	49.5	10.7	2222	1	A36028	DNA-directed DNA p	1201	49	10.6	366	2	G90951	probable cytochrom
1129	49.5	10.7	2403	2	T30875	PR8 protein homol	1202	49	10.6	367	2	G96770	hypothetical prote
1130	49.5	10.7	2500	1	W84UE2	HIV-Ep2 enhancer-b	1203	49	10.6	370	2	A80602	probable membrane
1131	49.5	10.7	3655	2	T38084	TRAP-11ike protein	1204	49	10.6	378	2	F64446	chorismate synthase
1132	49	10.6	98	2	T17363	NADH2 dehydrogenas	1205	49	10.6	379	2	B69332	heterodisulfide re
1133	49	10.6	99	2	T17177	NADH2 dehydrogenas	1206	49	10.6	380	2	T11033	ubiquinol-cytochro
1134	49	10.6	129	2	T28983	lsu ribosomal prot	1207	49	10.6	382	2	AH2056	hypothetical prote
1135	49	10.6	135	2	F86053	hypothetical prote	1208	49	10.6	385	2	A86227	hypothetical prote
1136	49	10.6	135	2	D91207	hypothetical prote	1209	49	10.6	391	2	T39673	probable mannosyl
1137	49	10.6	135	2	D91207	hypothetical prote	1210	49	10.6	396	2	T35024	probable glutathio
1138	49	10.6	137	1	A65171	ol15 protein - Bsc	1211	49	10.6	400	2	C83511	flagellar protein
1139	49	10.6	137	1	JC4877	phospholipase A2 h	1212	49	10.6	404	2	B86962	probable secreted
1140	49	10.6	140	2	S74898	hypothetical prote	1213	49	10.6	408	2	A37813	UDP-N-acetylglucos
1141	49	10.6	146	2	T06471	core protein - gar	1214	49	10.6	411	2	S75327	lysostaphin - Syne
1142	49	10.6	154	2	C71379	probable ATPase, c	1215	49	10.6	419	1	S47692	hypothetical 43.8k
1143	49	10.6	157	2	S18651	variant surface an	1216	49	10.6	419	2	B91169	probable transport
1144	49	10.6	157	2	S58025	probable olfactory	1217	49	10.6	419	2	B86015	hypothetical prote
1145	49	10.6	159	2	S77852	probable phenylala	1218	49	10.6	419	2	G70602	hypothetical prote
1146	49	10.6	160	2	S73261	plastocoulin-plast	1219	49	10.6	425	2	A64977	hypothetical prote
1147	49	10.6	163	2	D71062	hypothetical prote	1220	49	10.6	429	2	B87299	transporter, proba
1148	49	10.6	166	2	D82909	hypothetical prote	1221	49	10.6	431	1	E70699	probable pXa prot
1149	49	10.6	167	2	T11439	NADH2 dehydrogenas	1222	49	10.6	439	2	D72716	hypothetical prote
1150	49	10.6	167	2	B71553	hypothetical prote	1223	49	10.6	441	2	B82023	probable membrane
1151	49	10.6	167	2	A83204	hypothetical prote	1224	49	10.6	444	2	T24076	hypothetical prote
1152	49	10.6	169	2	B75490	hypothetical prote	1225	49	10.6	448	2	A70398	cell division prot
1153	49	10.6	170	2	H71937	3-dehydroquinatate d	1226	49	10.6	450	2	E69934	conserved hypothet
1154	49	10.6	170	2	F90050	hypothetical prote	1227	49	10.6	458	2	AC1173	amino acid transpo
1155	49	10.6	172	2	T33259	hypothetical prote	1228	49	10.6	458	2	AD1530	amino acid transpo
1156	49	10.6	172	2	E90617	NADH dehydrogenase	1229	49	10.6	463	2	C86042	probable transport
1157	49	10.6	179	1	ERAD34	early E3 20.1k gly	1230	49	10.6	463	2	B91195	probable transport
1158	49	10.6	181	2	JX0247	serine proteinase	1231	49	10.6	463	2	H65166	probable transport
1159	49	10.6	185	2	T41299	hypothetical metal	1232	49	10.6	463	2	H69822	sodium-glutamate s
1160	49	10.6	195	2	A82690	conserved hypothet	1233	49	10.6	466	2	G72603	nitrate reductase
1161	49	10.6	195	2	B97472	hypothetical prote	1234	49	10.6	469	1	AJBCQ	glutamate-ammonta
1162	49	10.6	196	2	T49023	hypothetical prote	1235	49	10.6	469	2	A83356	hypothetical prote
1163	49	10.6	196	2	G87510	hypothetical prote	1236	49	10.6	469	2	G86074	glutamine syntheta
1164	49	10.6	203	2	E72345	endopeptidase Clp	1237	49	10.6	469	2	H91227	glutamine syntheta
1165	49	10.6	203	2	T32745	hypothetical prote	1238	49	10.6	473	2	T07548	photosystem II chl
1166	49	10.6	205	2	T14744	hypothetical prote	1239	49	10.6	475	2	T36342	probable glutamate
1167	49	10.6	207	2	D75341	conserved hypothet	1240	49	10.6	475	2	T06061	cellulase (EC 3.2.
1168	49	10.6	212	2	AC0074	probable tellurium	1241	49	10.6	476	2	H96802	probable amino aci
1169	49	10.6	217	2	B90765	hypothetical prote	1242	49	10.6	485	2	G65051	phosphotransferase
1170	49	10.6	224	2	AG1795	hypothetical prote	1243	49	10.6	485	2	C91075	hypothetical prote
1171	49	10.6	236	2	E81406	hypothetical prote	1244	49	10.6	485	2	B85920	hypothetical prote
1172	49	10.6	244	2	S07398	gamma-gliadin B pr	1245	49	10.6	491	2	B71957	ATP-dependent RNA
1173	49	10.6	255	4	S31866	Ig gamma-1 chain C	1246	49	10.6	492	2	G64550	uroporphyrinogen-I
1174	49	10.6	262	2	T48546	hypothetical prote	1247	49	10.6	493	2	A11224	uroporphyrinogen-I
1175	49	10.6	263	2	A82559	transposase al1806	1248	49	10.6	493	2	AC1578	T-cell surface gly
1176	49	10.6	276	2	S73410	hypothetical prote	1249	49	10.6	495	1	A26396	probable transcrip
1177	49	10.6	287	2	E83928	transcription regu	1250	49	10.6	496	2	F83124	probable transcrip
1178	49	10.6	288	2	AH0247	transcription bindi	1251	49	10.6	507	2	UG0165	LARI protein - hum
1179	49	10.6	300	1	G75436	conserved hypothet	1252	49	10.6	510	2	S51124	probable membrane
1180	49	10.6	308	1	QRECM8	chemotaxis protein	1253	49	10.6	515	2	C58892	cytochrome-c oxida
1181	49	10.6	308	2	C85802	hypothetical prote	1254	49	10.6	516	2	T09949	cytochrome-c oxida
1182	49	10.6	308	2	G90953	chemotaxis protein	1255	49	10.6	522	1	IKEC1	Colicin EI - BscE
1183	49	10.6	308	2	H82936	hpr serine/threoni	1256	49	10.6	526	2	B65024	Hydrogenase-4 comp
1184	49	10.6	312	2	F87335	conserved hypothet	1257	49	10.6	535	2	D96586	hypothetical prote
1185	49	10.6	322	2	A12671	homoserine kinase	1258	49	10.6	542	2	C70732	probable integral
1186	49	10.6	324	1	JC4280	homoserine kinase	1259	49	10.6	553	1	H70786	probable dihydrol
1187	49	10.6	324	1	JC4280	carboxyl reductase	1260	49	10.6	555	2	S27163	alpha, alpha-trehal
1188	49	10.6	334	2	T16772	hypothetical prote	1261	49	10.6	557	2	A83040	urocanase (impor
1189	49	10.6	334	2	E87448	arginine-N-succiny	1262	49	10.6	573	2	G98245	hutu gene homolog
1190	49	10.6	335	2	T40292	glyceridehydride 3-p	1263	49	10.6	573	2	S28901	glutamate transpor
1191	49	10.6	337	1	Q0ECH3	probable dehydroge	1264	49	10.6	582	2	S22195	bps2 protein - Des
1192	49	10.6	337	2	C91029	probable PTS syste	1265	49	10.6	586	2	PC6006	scaffolding protei
1193	49	10.6	345	2	D85873	probable PTS syste	1266	49	10.6	597	2	S51212	BAXS protein - bov
1194	49	10.6	345	2	T28026	hypothetical prote	1267	49	10.6	602	2	E70067	conserved hypothet
1195	49	10.6	349	2	C86662	hypothetical prote	1268	49	10.6	605	2	D83007	regulatory protein
1196	49	10.6	352	2	A43113	chemokine (C-C) re	1269	49	10.6	616	2	AG2957	hypothetical prote
1197	49	10.6	353	2	H88939	protein CO5E4.13 (1270	49	10.6	616	2	G98325	probable c4-dicarb

1271	49	10.6	618	2	F84409
1272	49	10.6	629	2	S29685
1273	49	10.6	642	2	C84944
1274	49	10.6	660	2	T09537
1275	49	10.6	672	2	A65024
1276	49	10.6	672	2	D85891
1277	49	10.6	672	2	H91046
1278	49	10.6	680	2	T29871
1279	49	10.6	719	2	S63392
1280	49	10.6	740	2	T03847
1281	49	10.6	748	1	I50699
1282	49	10.6	784	2	JH0101
1283	49	10.6	796	2	E87636
1284	49	10.6	799	2	T48690
1285	49	10.6	812	2	AG3138
1286	49	10.6	812	2	D98149
1287	49	10.6	816	2	T21713
1288	49	10.6	839	2	S35319
1289	49	10.6	862	2	S64821
1290	49	10.6	952	2	E84534
1291	49	10.6	952	2	F71418
1292	49	10.6	969	2	T22788
1293	49	10.6	976	2	S40697
1294	49	10.6	1041	2	B81281
1295	49	10.6	1054	2	T30933
1296	49	10.6	1073	1	OYR0H4
1297	49	10.6	1086	2	T40354
1298	49	10.6	1190	2	T00842
1299	49	10.6	1207	2	T52459
1300	49	10.6	1230	2	S47466
1301	49	10.6	1265	2	T51314
1302	49	10.6	1366	2	S36851
1303	49	10.6	1430	2	AF0351
1304	49	10.6	1530	2	E82085
1305	49	10.6	1648	2	F84833
1306	49	10.6	2172	2	T20145
1307	49	10.6	3164	1	WMBEH6
1308	48.5	10.5	73	2	D91146
1309	48.5	10.5	73	2	H85991
1310	48.5	10.5	73	2	E65119
1311	48.5	10.5	75	2	T45361
1312	48.5	10.5	115	1	SPR8G
1313	48.5	10.5	116	2	AD2124
1314	48.5	10.5	139	2	G71033
1315	48.5	10.5	146	1	A47481
1316	48.5	10.5	165	2	A31635
1317	48.5	10.5	171	2	J50153
1318	48.5	10.5	180	2	T40562
1319	48.5	10.5	183	2	B81237
1320	48.5	10.5	183	2	G82008
1321	48.5	10.5	193	2	C97891
1322	48.5	10.5	198	2	S75989
1323	48.5	10.5	199	2	T38524
1324	48.5	10.5	199	2	A69855
1325	48.5	10.5	208	2	C39697
1326	48.5	10.5	211	2	C59091
1327	48.5	10.5	217	2	A98196
1328	48.5	10.5	221	2	D64907
1329	48.5	10.5	225	2	F81977
1330	48.5	10.5	225	2	A86043
1331	48.5	10.5	226	2	T23233
1332	48.5	10.5	235	2	AC2809
1333	48.5	10.5	235	2	H97587
1334	48.5	10.5	241	2	D84138
1335	48.5	10.5	243	2	B96010
1336	48.5	10.5	245	2	E97425
1337	48.5	10.5	245	2	A82643
1338	48.5	10.5	256	2	D86544
1339	48.5	10.5	257	2	H72078
1340	48.5	10.5	257	2	A12741
1341	48.5	10.5	257	2	H97522
1342	48.5	10.5	257	2	G87509
1343	48.5	10.5	258	2	H70487

arsenite transport	1344	48.5	10.5	269	2	G87134
retroviral recepto	1345	48.5	10.5	276	2	JS0172
threonine-tRNA lig	1346	48.5	10.5	276	2	D41044
xanthophyll epoxid	1347	48.5	10.5	277	2	D64666
hydrogenase-4 comp	1348	48.5	10.5	277	2	G71949
hydrogenase 4 memb	1349	48.5	10.5	278	2	AB2254
hydrogenase 4 memb	1350	48.5	10.5	283	2	B86331
hydrogenase 4 memb	1351	48.5	10.5	283	2	D71130
probable membrane	1352	48.5	10.5	290	2	F71167
Fae-binding protei	1353	48.5	10.5	291	2	F81444
cytosolic phosphol	1354	48.5	10.5	302	2	A75432
apolipoprotein B-1	1355	48.5	10.5	312	2	I40201
Tomb-dependent rec	1356	48.5	10.5	318	2	B91177
hypothetical prote	1357	48.5	10.5	330	2	C86023
fimbrial usher pro	1358	48.5	10.5	332	2	AC0260
hypothetical prote	1359	48.5	10.5	334	2	C81794
hypothetical prote	1360	48.5	10.5	340	2	E83126
nucleoporin-inte	1361	48.5	10.5	342	2	E71359
probable membrane	1362	48.5	10.5	355	2	T47527
hypothetical prote	1363	48.5	10.5	365	2	F87552
hypothetical prote	1364	48.5	10.5	370	2	AE0289
hypothetical prote	1365	48.5	10.5	372	2	C19371
processing endopro	1366	48.5	10.5	382	2	A10040
probable secreted	1367	48.5	10.5	387	2	H88012
chitinase (EC 3.2.	1368	48.5	10.5	388	2	T33908
heat-stable entero	1369	48.5	10.5	394	2	AE1940
hypothetical prote	1370	48.5	10.5	398	2	F75417
probable histidine	1371	48.5	10.5	400	2	AG1208
sensory transducti	1372	48.5	10.5	400	2	AB1565
cellulose 1,4-beta	1373	48.5	10.5	401	2	E72339
probable CO-induc	1374	48.5	10.5	406	2	T31778
L-shaped tail fibre	1375	48.5	10.5	409	2	B85735
glutamate autoctans	1376	48.5	10.5	410	2	C86835
glutamate synthase	1377	48.5	10.5	416	2	T02194
probable SNF2/SW12	1378	48.5	10.5	421	2	E90883
hypothetical prote	1379	48.5	10.5	424	2	T31978
U16 protein - hum	1380	48.5	10.5	425	2	T25873
hypothetical prote	1381	48.5	10.5	426	2	F45747
hypothetical prote	1382	48.5	10.5	426	2	T87853
hypothetical prote	1383	48.5	10.5	428	2	H01864
hypothetical prote	1384	48.5	10.5	431	2	J70721
substance P gamma	1385	48.5	10.5	436	2	T39973
hypothetical prote	1386	48.5	10.5	441	2	H89809
hypothetical prote	1387	48.5	10.5	443	2	H70430
interleukin-13 pre	1388	48.5	10.5	461	2	C98120
neural cell adhesi	1389	48.5	10.5	463	2	E81141
mitochondrial inne	1390	48.5	10.5	467	2	T32292
hypothetical 20.1K	1391	48.5	10.5	470	1	F2WU39
hypothetical prote	1392	48.5	10.5	473	2	T17260
probable integral	1393	48.5	10.5	475	2	T08753
hypothetical prote	1394	48.5	10.5	478	2	D64895
ATP synthase subun	1395	48.5	10.5	500	2	AD1047
hypothetical prote	1396	48.5	10.5	509	2	A96563
hypothetical prote	1397	48.5	10.5	510	2	E72007
protein K0289.4 [i	1398	48.5	10.5	511	2	H90439
hypothetical prote	1399	48.5	10.5	518	2	T05196
hypothetical prote	1400	48.5	10.5	528	2	E81186
membrane protein y	1401	48.5	10.5	537	2	A75123
hypothetical prote	1402	48.5	10.5	546	1	VGNZK
probable transposa	1403	48.5	10.5	546	2	S47305
conserved hypotnet	1404	48.5	10.5	553	2	C84920
conserved hypotnet	1405	48.5	10.5	553	2	T06499
hypothetical 25.1K	1406	48.5	10.5	556	2	S68408
hypothetical prote	1407	48.5	10.5	559	2	C75286
conserved hypotnet	1408	48.5	10.5	578	2	B82204
flagellar biosynth	1409	48.5	10.5	583	2	A70723
flagellar biosynth	1410	48.5	10.5	584	1	VCM51A
NADH (ubiquinone)	1411	48.5	10.5	590	2	C86465
conserved sodium-tr	1412	48.5	10.5	598	2	A66609
conserved hypotnet	1413	48.5	10.5	601	2	G96558
hypothetical prote	1414	48.5	10.5	605	2	T15291
hypothetical prote	1415	48.5	10.5	608	2	C95255
cytochrome-c oxida	1416	48.5	10.5	610	2	A11110

enoyl-[ACP] reduct	enoyl-1 a/b-bi	octopine-binding p	glutamine ABC tran	amino acid ABC tra	hypothetical prote	Fe69.15 protein -	probable oligopept	hypothetical prote	probable integral	3-hydroxybutyryl-C	meu protein - Bac	probable hemin per	hypothetical phage	hypothetical prote	hypothetical prote	ferric enterobacti	hypothetical prote	hypothetical prote	gpIIA protein (limp	conserved hypotnet	Ig V-region-like B	probable methanol	protein K1084.2 [i	hypothetical prote	two-component resp	L-sorbose dehydr	cell-division prot	cell-division prot	hypothetical prote	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	UDP-N-acetylglucos	hypothetical prote	hypothetical 47.0K	probable esterase	alkaline serine pr	K+ transport prote	glycerol-3-phospha	xanthine/uracil pe	hypothetical prote	IL2 protein - human	hypothetical prote	hypothetical prote	probable membrane	probable amino aci	conserved hypotnet	hypothetical prote	L-lactate permease	proline permease (cell fusion glycop	gene F protein - r	hypothetical prote	Rieske [2Fe-2S] ir	aplysin A precu	hypothetical prote	methyI-accepting c	probable acyl-coAS	env polyprotein pr	probable inositol	carbon starvation	probable protein k	spingomyelin phos	hypothetical prote	two-component sens
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R.Mercer, R.W.; Blomstedter, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
 J. Cell Biol. 121, 579-586, 1993
 A:Title: Molecular cloning and immunological characterization of the gamma polypeptide,
 A:Reference number: A6435; MUID:9325293; PMID:8387529
 A:Accession: B6435

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-58 <MER>
 A:Cross-references: UNIPROT:004679; UNIPARC:UPI0000170985; EMBL:X70062; NID:956299; PIDN
 A:Note: the authors translated the codon TTC for residue 25 as Pro
 C:Keywords: hydrolase; transmembrane protein

Query Match 16.4%; Score 75.5; DB 2; Length 58;
 Best Local Similarity 34.7%; Pred. No. 0.19;
 Matches 17; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

Qy 27 DDPFYDMKNLQSLGICGLAIAVLSGCKYKSSOKOHPVE 75
 Db 8 ENPFYDYETVAKGGLIFAGLAFVVGILLISKRRFCGS-KKHQVNE 55

RESULT 8

Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: C46435; S1522

R.Mercer, R.W.; Blomstedter, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
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A:Title: Molecular cloning and immunological characterization of the gamma polypeptide,
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A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-58 <MER>
 A:Cross-references: UNIPROT:004646; UNIPARC:UPI00001482CD; EMBL:X70060; NID:951111; PIDN
 A:Note: the authors translated the codon TTC for residue 25 as Pro
 C:Keywords: hydrolase; transmembrane protein

Query Match 15.9%; Score 73.5; DB 2; Length 58;
 Best Local Similarity 32.7%; Pred. No. 0.32;
 Matches 16; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

Qy 27 DDPFYDMKNLQSLGICGLAIAVLSGCKYKSSOKOHPVE 75
 Db 8 ENPFYDYETVAKGGLIFAGLAFVVGILLISKRRFC-GGKHKHQQVNE 55

RESULT 9

A61088
 plastocyanin-plastocyanin reductase (EC 1.10.99.1) 17K protein - Synechocystis sp. (sera
 N:Alternate names: cytochrome b6-f complex chain IV; plastocyanin-plastocyanin reductase
 C:Species: Synechocystis sp.

A:Variety: PCC 6803
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A61088; S76298; S15474

R.Ostlewar, H.D.
 Arch. Microbiol. 157, 336-342, 1992
 A:Title: Construction of insertion mutants of Synechocystis sp. PCC 6803: evidence for a
 A:Reference number: A61088; MUID:92272582; PMID:1590707
 A:Accession: A61088

A:Molecule type: DNA
 A:Residues: 1-160 <SKI>
 A:Cross-references: UNIPROT:P27589; UNIPARC:UPI0000131690; EMBL:X58522; NID:947376; PIDN
 R.Kanehko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76298
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-160 <KAN>
 A:Cross-references: UNIPARC:UPI0000131690; EMBL:D64000; GB:AB001339; NID:91001484; PIDN:
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics: petD
 C:Superfamily: cytochrome b6-f complex, subunit 4 (plastocyanin-plastocyanin reductase,
 C:Keywords: oxidoreductase; photosynthesis; thylakoid
 F.24-144/Domain: plastocyanin-plastocyanin reductase 17K protein homology <17K>

Query Match 15.6%; Score 72; DB 1; Length 160;
 Best Local Similarity 37.7%; Pred. No. 1.4;
 Matches 23; Conservative 9; Mismatches 21; Indels 8; Gaps 2;

Qy 7 ALLTAGLTAI-----EANDPFANKD--PFYDMKNLQSLGICGLAIAVLS 58
 Db 47 ALGAGLAILDPMNIGPADPFPATPLELDEWYLPFFQILRIIPNLTLGAGWAAIPL 106

Qy 59 G 59
 Db 107 G 107

RESULT 10

F69989
 conserved hypothetical protein ytcD - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: F69989

R.Kunst, F.; Ogatawa, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gallier
 tech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
 Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
 akouchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumeitein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: F69989
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-529 <KUN>
 A:Cross-references: UNIPROT:O34355; UNIPARC:UPI0000608E4; GB:Z99119; GB:AL009126; NID:9
 A:Experimental source: strain 168
 C:Genetics: ytcD

Query Match 15.4%; Score 71; DB 2; Length 529;
 Best Local Similarity 30.4%; Pred. No. 6.2;
 Matches 31; Conservative 9; Mismatches 24; Indels 38; Gaps 6;

Qy 16 ALBANDPFANKDPPYD-----WKNLQSLGICG-----LLAING 52
 Db 381 ALDLPHPVASFPPVIVIRLKGDKRMKTAFAWTLTISKGLCGSGSDAPIPVDPGLIQ- 439

Qy 53 IAAVLSGCKYKSSOKOHP-----VP-EKAIPLIRGSA 86
 Db 440 -SAVLR-----KSHQNGPSTNESECIPEYAIKLTIEGSA 475

RESULT 11

AH0371
 probable membrane protein ypo3057 (imported) - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AH0371
 R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AH0371
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-150 <KUR>
A/Cross-references: UNIPROT:Q8ZCD4, UNIPARC:UPI00000CD9C4, GB:AL590842; PIDN:CAC92299.1;
C/Genetics:
A/Gene: YPO3057
C/Superfamily: hypothetical protein yrcW

Query Match 15.0%; Score 69; DB 2; Length 150;
Best Local Similarity 30.2%; Pred. No. 2.7;
Matches 26; Conservative 14; Mismatches 32; Indels 14; Gaps 4;
Oy 4 VTLALLAGLTALBPANKDDPFYDMKNLQSLGICGGLAIAAGT-AAVLSGKCK 62
Db 26 VTLAILLILAIIRTPPLNS-----FFPW--VEKGLITIGVILITIGVWAPIASG--K 72

Oy 63 YKSQKOHSPYPEKAIPLITPGSAT 88
Db 73 ISASEVLSHFYQWKSILAIIVGVAVS 98

RESULT 12
A05009
hypothetical protein 135 - liverwort (Marchantia polymorpha) chloroplast
C/Species: chloroplast Marchantia polymorpha
C/Date: 05-Jun-1997 #sequence_revision 05-Jun-1997 #text_change 09-Jul-2004
C/Accession: S01571; A05009
R/Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T
J. Mol. Biol. 203, 299-331, 1998
A>Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gen
A/Reference number: S01567; MUID:8906866; PMID:2974085
A/Accession: S01571
A/Molecule type: DNA
A/Residues: 1-135 <UME>
A/Cross-references: UNIPROT:Q32616; UNIPARC:UPI000013A518; EMBL:X04465; NID:g11640; PIDN
R; Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A>Title: Chloroplast gene organization deduced from complete sequence of liverwort March
A/Reference number: A38014
A/Contents: annotation; gene organization, sites, features
C/Genetics:
A/Genome: chloroplast
A/Intons: 36/1
C/Superfamily: hypothetical protein 135
C/Keywords: chloroplast

Query Match 14.6%; Score 67.5; DB 2; Length 135;
Best Local Similarity 33.6%; Pred. No. 3.6;
Matches 15; Conservative 11; Mismatches 13; Indels 7; Gaps 2;
Oy 9 LTLAANDPANKDDPFYDMKNLQSLGICGGLAIAAG 52
Db 16 LITIGLFLYALKLRPEYSRDYDFFF---SCIGLIGGLIFPG 56

RESULT 13
B86620
choirismate synthase [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86620
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86491; MUID:20303049; PMID:10871362
A/Accession: B86620
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-359 <STO>
A/Cross-references: UNIPROT:Q9Z6M2; UNIPARC:UPI0000125F94; GB:BA000008; NID:g8979410; PII
A/Experimental source: strain J138
C/Genetics:
A/Gene: aroC
C/Superfamily: choirismate synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;
Oy 7 ALLIAGLTALBPANKD-----DPFYDMKNLQSLGICGGLAIAAGTAAVLSG 59
Db 234 ALMSIPAKFPIGKGFASQMGSGYTDPFVWEGENITLKSNNCGGLTIGITGVPIEG 293

Oy 60 KCKYK--SSOK-----QHSP-VPEKAIPLI 81
Db 294 RIAFKPTSSIKRPGCATVTKTKETTYRTPQGRHDPVCAIRAVPVV 339

RESULT 14
A72004
choirismate synthase CP0815 [imported] - Chlamydia pneumoniae (strains CWL029 and AR3
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: A72004; D81536
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Ollinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; MUID:99206606; PMID:10192388
A/Accession: A72004
A/Molecule type: DNA
A/Status: preliminary
A/Cross-references: UNIPROT:Q9Z6M2; UNIPARC:UPI0000125F94; GB:AE001684; GB:AE001363; NID
A/Experimental source: strain CWL029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis Mohn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: D81536
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <REA>
A/Cross-references: UNIPARC:UPI0000125F94; GB:AE002240; GB:AE002161; NID:g7189720; PIDN:
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: aroC; CP0815
C/Superfamily: choirismate synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;
Oy 7 ALLIAGLTALBPANKD-----DPFYDMKNLQSLGICGGLAIAAGTAAVLSG 59
Db 234 ALMSIPAKFPIGKGFASQMGSGYTDPFVWEGENITLKSNNCGGLTIGITGVPIEG 293

Oy 60 KCKYK--SSOK-----QHSP-VPEKAIPLI 81
Db 294 RIAFKPTSSIKRPGCATVTKTKETTYRTPQGRHDPVCAIRAVPVV 339

RESULT 15
A8101
potassium channel KCNA3 - human
A/Alternate names: potassium channel HLK3; potassium channel PCN3; shaker-related potase
C/Species: Homo sapiens (hmn)
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: A8101; B38556; J52990
R/Attali, B.; Romey, G.; Honore, E.; Schmid-Aliana, A.; Mattei, M.G.; Lesage, F.; Ricar

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OM protein - protein search, using sw model

Run on: December 14, 2005, 06:25:35 ; Search time 171 Seconds
(without alignments)
367.205 Million cell updates/sec

Title: US-10-063-557-50

Perfect score: 461
Sequence: 1 MERVTLALLAGLTAEAN.....HSPVPEKAIPIITPGSARTTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	2	Q6UWZ1 HUMAN
2	452	98.0	89	2	Q7Z4M5 HUMAN
3	450	97.6	88	1	FXVD4 HUMAN
4	276.5	60.0	88	1	FXVD4_MOUSE
5	256.5	55.6	87	1	FXVD4_RAT
6	241.5	52.4	88	1	FXVD3_MOUSE
7	234.5	50.9	88	1	FXVD3_RAT
8	230.5	50.0	88	1	FXVD3_MOUSE
9	214.5	46.5	87	1	FXVD3_HUMAN
10	214.5	46.5	87	2	Q6IB59 HUMAN
11	203	44.0	70	2	Q80UV3 MOUSE
12	129	28.0	92	1	PLM HUMAN
13	127.5	27.7	88	2	Q4RFQ2 TETNG
14	126.5	27.4	92	1	PLM CANFA
15	124.5	27.0	94	1	FXVD6_RAT
16	123.5	26.8	94	1	FXVD6_MOUSE
17	119	25.8	100	2	Q5M8E9 XENTR
18	116	25.2	94	2	Q70012 SQUAC
19	115.5	25.1	92	1	PLM MOUSE
20	115	24.9	95	1	FXVD6_PONPY
21	113.5	24.6	95	2	Q6D7F4 XENLA
22	113	24.5	92	1	PLM RAT
23	112.5	24.4	95	1	FXVD6_HUMAN
24	112.5	24.4	95	1	FXVD6_MOUSE
25	110	23.9	95	2	Q5ZM59 CHICK
26	107.5	23.3	94	2	Q4RHT7 TETNG
27	103.5	22.5	94	2	Q6D7D6 XENLA
28	96.5	20.9	58	1	ATNG_BOVIN
29	96	20.8	99	2	Q7S252 BRARE
30	95.5	20.7	53	1	ATNG SHEEP
31	95.5	20.7	65	2	Q5K79_PIG

32	94	20.4	178	1	FXVD5 HUMAN	Q96D9 homo sapien
33	92	20.0	178	1	FXVD5_RAT	P5867 ratu
34	92	20.0	178	1	Q6P9W0 RAT	Q6P9W0 ratu
35	89	19.3	80	1	FXVD7 HUMAN	P58549 homo sapien
36	85	18.4	80	1	FXVD7_MOUSE	P58648 mus musculi
37	84	18.2	178	2	Q8IWS1 HUMAN	Q8IWS1 homo sapien
38	83	18.0	66	1	ATNG_HUMAN	P54710 homo sapien
39	83	18.0	80	1	FXVD7_RAT	P58649 ratu
40	83	18.0	94	1	FXVD8 HUMAN	P58550 homo sapien
41	82.5	17.9	66	1	ATNG_RAT	Q04679 ratu
42	79.5	17.2	142	2	Q6P8R9 MOUSE	Q6P8R9 mus musculi
43	78	16.9	70	1	ATNG_MOUSE	Q04646 mus musculi
44	78	16.9	70	2	Q6IT12_MOUSE	Q6IT12 mus musculi
45	77.5	16.8	711	2	Q4NGJ7_GNICC	Q4NGJ7 athricobacte
46	76	16.5	289	2	Q4WU10 ASPFC	Q4WU10 aspergillus
47	75.5	16.4	524	2	Q5LOV1_SILPO	Q5LOV1 silicibacte
48	74	16.1	188	2	Q5IM65_SILPO	Q5IM65 silicibacte
49	74	16.1	208	2	Q4RE60_MACFA	Q4RE60 macaca fasc
50	73.5	15.9	64	2	Q6IT11_MOUSE	Q6IT11 mus musculi
51	73.5	15.9	82	2	Q6IT10_MOUSE	Q6IT10 mus musculi
52	73.5	15.9	196	2	Q9GZET_CAEEL	Q9GZET caenorhabdi
53	73.5	15.9	330	2	Q84EY9_ENTCL	Q84EY9 enterobacte
54	73.5	15.8	201	2	Q7QJ63_ANOGA	Q7QJ63 anophelle
55	73	15.8	455	2	Q4IPU0_GIBZV	Q4IPU0 gibbelle
56	73	15.8	1132	2	Q83861_9REOV	Q83861 nilaparvata
57	72	15.8	1343	2	Q521Q6_MAGGR	Q521Q6 magnaporthe
58	72	15.6	160	1	PETD_SYNY3	P27589 synechocyst
59	71	15.4	61	1	ATNG_XENLA	Q13001 xenopus lae
60	71	15.4	529	2	Q34355_BACSU	Q34355 bacillus su
61	70.5	15.3	251	2	Q4F08_DICDI	Q4F08 dictyosteli
62	70.5	15.3	334	2	Q6D644_ERWCT	Q6D644 erwinta car
63	70	15.2	184	1	FXVD5_MOUSE	P97808 mus musculi
64	70	15.2	216	2	Q5ZFE6_PLAMJ	Q5ZFE6 plantago lae
65	69.5	15.1	236	2	Q6GME4_XENLA	Q6GME4 xenopus lae
66	68.5	15.1	268	2	Q4FSL8_9GAMM	Q4FSL8 psychrobact
67	69.5	15.1	458	2	Q5KUP7_GEOKA	Q5KUP7 geobact
68	69	15.0	150	2	Q668G1_YERPE	Q668G1 yerisinda pe
69	69	15.0	157	2	Q8ZCDA_YERPE	Q8ZCDA yerisinda pe
70	69	15.0	150	2	Q8DOY1_YERPE	Q8DOY1 yerisinda pe
71	68.5	14.9	340	2	Q9LUR6_ARATH	Q9LUR6 arabidopsis
72	68.5	14.9	349	2	Q94E19_ARATH	Q94E19 arabidopsis
73	68.5	14.9	456	2	Q9CLJ0_PASMU	Q9CLJ0 pasteurella
74	68.5	14.9	485	2	Q5BEX5_BRARE	Q5BEX5 brachydanto
75	68.5	14.9	499	2	Q5VHU4_CIOIN	Q5VHU4 cloina inter
76	68.5	14.9	531	2	Q5VHU5_CIOIN	Q5VHU5 cloina inter
77	68	14.8	173	2	Q8HKR3_9PERC	Q8HKR3 arcos sp. k
78	68	14.8	417	2	Q4QD23_LEIMA	Q4QD23 leishmania
79	68	14.8	978	2	Q6S9P5_ORYSA	Q6S9P5 oryza sativ
80	67.5	14.6	135	1	YCF66_MARPO	Q32616 marchantia
81	67.5	14.6	337	2	Q6L3V4_SOLDE	Q6L3V4 solanum dem
82	67.5	14.6	387	2	Q6YXY7_ORYSA	Q6YXY7 oryza sativ
83	67.5	14.6	664	2	Q75485_HUMAN	Q75485 homo sapien
84	67.5	14.6	664	2	Q8WU17_HUMAN	Q8WU17 homo sapien
85	67.5	14.6	664	2	Q5RBT7_PONPY	Q5RBT7 pongo pygma
86	67	14.5	364	1	Q5XF87_PLAMJ	Q5XF87 plantago ma
87	67	14.5	390	1	AROC_SILURO	Q96Y94 sulfolobus
88	67	14.5	715	2	Q72E54_DESVH	Q72E54 desulfobact
89	66.5	14.4	198	2	Q51VA7_MAGGR	Q51VA7 magnaporthe
90	66.5	14.4	241	2	Q9K313_STRCO	Q9K313 streptomyce
91	66.5	14.4	329	2	Q6ODJ9_SOLTU	Q6ODJ9 solanum tub
92	66.5	14.4	359	1	AROC_CHLPN	Q946M2 chlamydia p
93	66.5	14.4	516	2	Q28656_RABIT	Q28656 coryctolaqu
94	66.5	14.4	523	1	KCMA3_HUMAN	P22001 homo sapien
95	66.5	14.4	546	2	Q5RA50_PONPY	Q5RA50 pongo pygma
96	66.5	14.4	549	2	Q8B9W6_SHEON	Q8B9W6 shewanella
97	66.5	14.4	557	2	Q6P2D3_HUMAN	Q6P2D3 homo sapien
98	66.5	14.4	575	2	Q5VWN2_HUMAN	Q5VWN2 homo sapien
99	66	14.3	139	2	Q5XWNO_SOLTU	Q5XWNO solanum tub
100	66	14.3	446	2	Q87UY7_SILURO	Q87UY7 sulfolobus
101	65.5	14.2	161	2	Q5SN36_CRYNE	Q5SN36 cryptococcu
102	65.5	14.2	161	2	Q5KB35_CRYNE	Q5KB35 cryptococcu
103	65.5	14.2	305	2	Q74DY6_GEOSL	Q74DY6 geobacter s
104	65.5	14.2	333	2	Q6L3P2_SOLDE	Q6L3P2 solanum dem

105	65.5	14.2	546	2	Q96N93_HUMAN	Q96n19 homo sapien	178	63	13.7	467	2	Q41SE1_GIBBEZ	Q41s61 gibberella
106	65.5	14.2	546	2	Q96V42_HUMAN	Q96v42 homo sapien	179	63	13.7	468	2	Q92VA7_ARATH	Q92v87 arabidopsis
107	65.5	14.2	582	2	Q98B89_HUMAN	Q98b89 homo sapien	180	63	13.7	496	2	Q7NB28_MYCQA	Q7nb28 mycoplasma
108	65.5	14.2	1185	2	Q98G58_SHEON	Q98g58 shewanella	181	63	13.7	622	2	Q590Y3_CANAL	Q59y3 candida alb
109	65.5	14.2	1278	2	Q4SM90_TETNG	Q4sm90 tetracodon n	182	63	13.7	655	2	Q8KW93_STRMU	Q8kw93 streptococc
110	65	14.1	1344	2	Q5R157_BRARE	Q5r157 brachydanio	183	63	13.7	655	2	Q8DUN3_STRMU	Q8dun3 streptococc
111	65	14.1	327	2	Q91V63_ARATH	Q91v63 arabidopsis	184	63	13.7	750	2	Q59R09_CANAL	Q59r09 candida alb
112	65	14.1	427	2	Q4UV91_THAAT	Q4uv91 theileria a	185	63	13.7	808	2	Q6DD69_XENLA	Q6dd69 xenopus lae
113	65	14.1	469	2	Q9XDX1_MAGMG	Q9xdx1 magnecospir	186	63	13.7	825	2	Q993G5_9GAMA	Q993g5 gallitrichi
114	65	14.1	582	2	Q5UQ22_MIMIV	Q5uq22 mimivirius	187	63	13.7	912	2	Q8D4M3_VIBVU	Q8d4m3 vibrio vuln
115	65	14.1	760	2	Q9P638_CHICK	Q9p638 gallus gall	188	63	13.7	917	2	Q5E8X2_VIBF1	Q5e8x2 vibrio fisc
116	65	14.1	832	2	Q4SB80_TETNG	Q4sb80 tetracodon n	189	63	13.7	923	2	Q9N389_CAEEL	Q9n389 caenorhabdi
117	64.5	14.0	155	2	Q9R126_MOUSE	Q9r126 mus musculu	190	63	13.7	1022	2	Q27779_SCHNA	Q27779 schistosoma
118	64.5	14.0	189	2	Q6C1N8_YARLI	Q6c1n8 yarrowia l1	191	63	13.7	1411	2	Q5AS38_EMEIN	Q5as38 aspergillus
119	64.5	14.0	244	2	Q7ZEX5_DESVH	Q7zex5 desulfocovbr	192	62.5	13.6	146	2	Q81GV1_BACCR	Q81gv1 bacillus ce
120	64.5	14.0	311	2	Q4HB57_9DEIO	Q4hb57 deinococcus	193	62.5	13.6	160	2	Q8PFE0_SCHJA	Q8pfe0 schistosoma
121	64.5	14.0	312	2	Q71Y12_LISMP	Q71y12 listeria mo	194	62.5	13.6	163	2	Q73CB6_BACCT	Q73cb6 bacillus ce
122	64.5	14.0	372	2	Q5WM34_LEGPE	Q5wm34 legionella	195	62.5	13.6	207	2	Q8TBL6_HUMAN	Q8tbl6 homo sapien
123	64.5	14.0	452	2	Q7T165_BRARE	Q7t165 brachydanio	196	62.5	13.6	286	2	Q9BSB3_HUMAN	Q9bsb3 homo sapien
124	64.5	14.0	455	2	Q8TX25_PYRFU	Q8tx25 pyrococcus	197	62.5	13.6	299	1	COMO_BACSU	Q33630 bacillus su
125	64.5	14.0	455	2	Q9E080_RHOSH	Q9e080 rhodobacter	198	62.5	13.6	303	2	Q9UNZ3_HUMAN	Q9unz3 homo sapien
126	64.5	14.0	550	2	Q9GEM7_9PARA	Q9gem7 measles vir	199	62.5	13.6	339	2	Q53HB8_HUMAN	Q53hb8 homo sapien
127	64.5	14.0	550	2	Q9GEM9_9PARA	Q9gem9 measles vir	200	62.5	13.6	339	2	Q96BY9_HUMAN	Q96by9 homo sapien
128	64.5	14.0	633	2	Q4SHG0_TETNG	Q4shg0 tetracodon n	201	62.5	13.6	339	2	Q916B3_HUMAN	Q916b3 homo sapien
129	64.5	14.0	677	2	Q5GU05_XANOR	Q5gu05 xanthomonas	202	62.5	13.6	372	2	Q5ZUY1_LEGPH	Q5zuy1 legionella
130	64.5	14.0	725	2	Q98Y05_DROME	Q98y05 drosophila	203	62.5	13.6	434	2	Q6HH27_BACHK	Q6hh27 bacillus th
131	64.5	14.0	871	2	Q5A4X3_CANAL	Q5a4x3 candida alb	204	62.5	13.6	434	2	Q81PR7_BACAN	Q81pr7 bacillus an
132	64.5	14.0	920	2	Q6XR97_9BACT	Q6xr97 uncultured	205	62.5	13.6	492	2	Q750E3_ASHGO	Q750e3 ashyba gose
133	64.5	14.0	1750	2	Q4WR93_ASPTU	Q4wr93 aspergillus	206	62.5	13.6	504	2	Q7S9U0_NEUCR	Q7s9u0 neurospora
134	64	13.9	186	2	Q4RH15_TETNG	Q4rh15 tetracodon n	207	62.5	13.6	525	2	Q76235_TRYCO	Q76235 trypanosoma
135	64	13.9	250	2	Q7WU64_9THEM	Q7wu64 thermotoga	208	62.5	13.6	525	2	Q9NC29_TRYCO	Q9nc29 trypanosoma
136	64	13.9	303	2	Q4KGC4_PSEBF	Q4kgc4 pseudomonas	209	62.5	13.6	539	2	Q9RD59_STRCO	Q9rd59 streptomyces
137	64	13.9	315	2	Q9LS88_ARATH	Q9ls88 arabidopsis	210	62.5	13.6	557	2	Q7XQW8_ORYSA	Q7xqw8 oryza sativ
138	64	13.9	340	2	Q7ZM35_LEPIC	Q7zm35 leptospira	211	62.5	13.6	580	2	Q5T6S3_HUMAN	Q5t6s3 homo sapien
139	64	13.9	383	2	Q6R5J0_RHORA	Q6r5j0 rhodopseudo	212	62.5	13.6	604	2	Q9VNP7_DROME	Q9vnp7 drosophila
140	64	13.9	436	2	Q86VR7_HUMAN	Q86vr7 homo sapien	213	62.5	13.6	621	2	Q6N038_HUMAN	Q6n038 homo sapien
141	64	13.9	525	1	KCNM33_RAT	P13384 rattus norv	214	62.5	13.6	663	2	Q72PX8_LEPIC	Q72px8 leptospira
142	64	13.9	582	2	Q6K620_ORYSA	Q6k620 oryza sativ	215	62.5	13.6	663	2	Q8F6A7_LEPIN	Q8f6a7 leptospira
143	64	13.9	667	2	Q9BJM1_TRISP	Q9bjm1 trichinella	216	62.5	13.6	670	2	Q4SQ15_TETNG	Q4sq15 tetracodon n
144	64	13.9	678	2	Q8R9G1_THETN	Q8r9g1 thelmoaner	217	62.5	13.6	685	2	Q8EEB6_SHEON	Q8eeb6 shewanella
145	64	13.9	727	2	Q6F1K3_CANCA	Q6f1k3 candida gla	218	62.5	13.6	700	2	Q8TG00_ASPTU	Q8tg00 aspergillus
146	64	13.9	804	2	Q75GV0_ORYSA	Q75gv0 oryza sativ	219	62.5	13.6	700	2	Q4W8B9_ASPTU	Q4w8b9 aspergillus
147	64	13.9	915	2	Q7MG71_VIBVU	Q7mg71 vibrio vuln	220	62.5	13.6	760	2	Q7XNUS_ORYSA	Q7xnus oryza sativ
148	64	13.9	1046	2	Q82WK5_NITEU	Q82wk5 nitrobomona	221	62.5	13.6	769	1	KCNK3_ORYSA	Q63395 mus musculu
149	63.5	13.8	241	2	Q5UX90_HALMA	Q5ux90 haloarcula	222	62.5	13.6	850	2	Q65M95_BACLD	Q65m95 bacillus l1
150	63.5	13.8	309	2	Q8Y5P7_LISMO	Q8y5p7 listeria mo	223	62.5	13.6	910	1	SYL_NEIMA	Q93w39 neisseria m
151	63.5	13.8	309	2	Q92A05_LISIN	Q92a05 listeria in	224	62.5	13.6	1048	1	SIL1_SALTY	Q93h69 salmonella
152	63.5	13.8	318	2	Q4TG61_GIBZE	Q4tg61 gibberella	225	62.5	13.6	1048	2	Q6MXQ0_SERMA	Q6mxq0 seretia ma
153	63.5	13.8	327	2	Q6ZVM5_HUMAN	Q6zvm5 homo sapien	226	62	13.4	179	1	DSBB_HABDU	Q893n4 clostridium
154	63.5	13.8	359	2	Q822F8_CHICV	Q822f8 chlamydomo	227	62	13.4	189	2	Q6X9L3_SULIS	Q6x9l3 haemophilus
155	63.5	13.8	372	2	Q5X4P4_LEGPA	Q5x4p4 legionella	228	62	13.4	269	2	Q6WYM5_ORYSA	Q6wy5 oryza sativ
156	63.5	13.8	396	2	Q5UUV7_9PEZI	Q5uvu7 cercophora	229	62	13.4	308	2	Q61BX8_CABER	Q61bx8 caenorhabdi
157	63.5	13.8	410	2	Q4LUJ0_9BURK	Q4luj0 burkholderi	230	62	13.4	308	2	Q8BRU1_MOUSE	Q8bru1 mouse
158	63.5	13.8	420	2	Q6T5E8_ORYSA	Q6t5e8 oryza sativ	231	62	13.4	308	2	Q8UC07_AGR75	Q8uc07 agrotacteri
159	63.5	13.8	452	2	Q6FVH0_CANCA	Q6fvh0 candida gla	232	62	13.4	381	2	Q7CMG7_AGR75	Q7cmg7 agrotacteri
160	63.5	13.8	511	1	KCNK1_HUMAN	P15388 mus musculu	233	62	13.4	393	2	Q323B3_STRGR	Q323b3 streptomyces
161	63.5	13.8	511	1	KCNK1_MOUSE	Q5n338 mus musculu	234	62	13.4	414	2	Q7XTD2_ORYSA	Q7xtd2 oryza sativ
162	63.5	13.8	511	2	Q5BN35_RABIT	Q5bn35 oryctolagus	235	62	13.4	419	2	Q96Y94_SULTO	Q96y94 sulfolobus
163	63.5	13.8	511	2	Q5BN36_BOVIN	Q5bn36 bos taurus	236	62	13.4	445	2	Q8PHR1_XANNC	Q8phr1 xanthomonas
164	63.5	13.8	521	2	Q4V7K2_XENLA	Q4v7k2 xenopus lae	237	62	13.4	470	2	Q65UC0_NANSM	Q65uc0 nanneimela
165	63.5	13.8	550	2	Q9GEM8_9PARA	Q9gem8 measles vir	238	62	13.4	489	2	Q8N1V9_HUMAN	Q8n1v9 homo sapien
166	63.5	13.8	585	1	KCNK1_RAT	P25122 rattus norv	239	62	13.4	558	2	Q9V7C4_DROME	Q9v7c4 drosophila
167	63.5	13.8	585	2	Q9XSJ8_CANFA	Q9xsj8 canis famli	240	62	13.4	577	2	Q4LEB7_HUMAN	Q4leb7 homo sapien
168	63.5	13.8	620	2	Q7U2A5_MYCBO	Q7u2a5 mycobacteri	241	62	13.4	581	1	FURA_SCHPO	Q51502 pseae
169	63.5	13.8	620	2	Q07239_MYCTU	Q07239 mycobacteri	242	62	13.4	613	2	Q96P50_HUMAN	Q96p50 schistosach
170	63.5	13.8	642	2	Q4SZN6_TETNG	Q4szn6 tetracodon n	243	62	13.4	629	2	Q86R09_HUMAN	Q86r09 homo sapien
171	63.5	13.8	725	2	Q5HL36_CANLA	Q5hl36 campylobact	244	62	13.4	631	2	Q96PR1_HUMAN	Q96pr1 homo sapien
172	63.5	13.8	747	2	Q575Z7_MAIZE	Q575z7 zea mays (m	245	62	13.4	648	2	Q4LEB7_HUMAN	Q4leb7 homo sapien
173	63	13.7	80	2	Q7NUJ3_CHRVO	Q7nuj3 chromobace	246	62	13.4	777	2	Q51502_PSEAE	Q51502 pseudomonas
174	63	13.7	125	2	Q5J1J3_PYRKO	Q5j1j3 pyrococcus	247	62	13.4	862	2	Q6MYC9_ASPTU	Q6myc9 aspergillus
175	63	13.7	201	2	Q5NSMO_SYNRP	Q5nsmo syntrophoc	248	62	13.4	862	2	Q4WS92_ASPTU	Q4ws92 aspergillus
176	63	13.7	378	2	Q7OFG1_ANOGA	Q7ofg1 anopheles g	249	62	13.4	962	2	Q6BZ68_DBBHA	Q6bz68 debaryomyces
177	63	13.7	465	2	Q4PDK1_USTMA	Q4pdk1 ustilago ma	250	62	13.4	1025	2	Q4QGS8_LEIMA	Q4qgs8 leishmania

251	62	13.4	1057	2	Q6FT12_CANGA	Q6FT12 candida gla	324	61	13.2	413	2	Q59KD6_CANAL	Q59KD6 candida alb
252	62	13.3	2325	2	Q9N3X8_CABEL	Q9N3X8 caenorhabdi	325	61	13.2	461	2	Q9SSF6_ECOLI	Q9SSF6 escherichia
253	61.5	13.3	134	2	Q6RSM0_9BACI	Q6RSM0 bacillus sp	326	61	13.2	461	2	Q7ACQ0_ECO57	Q7ACQ0 escherichia
254	61.5	13.3	178	2	Q83E78_COXBU	Q83E78 coxiella bu	327	61	13.2	463	2	Q9V1R1_PYRAB	Q9V1R1 pyrococcus
255	61.5	13.3	180	2	Q6T5E4_CORSA	Q6T5E4 oryza sativ	328	61	13.2	463	2	Q59471_PYRHO	Q59471 pyrococcus
256	61.5	13.3	206	2	Q5UELE_PYRKO	Q5UELE pyroco	329	61	13.2	463	2	Q85337_ECOLI	Q85337 escherichia
257	61.5	13.3	210	2	Q636E4_BACCF	Q636E4 bacillus ce	330	61	13.2	463	2	Q7DFR2_ECO57	Q7DFR2 escherichia
258	61.5	13.3	213	2	Q6RFR7_CORF	Q6RFR7 corynbacte	331	61	13.2	484	2	Q5GXA1_XANOR	Q5GXA1 xanthomonas
259	61.5	13.3	216	2	Q4MJU0_9MICC	Q4MJU0 archirocto	332	61	13.2	488	2	Q5Z1J6_NOCFA	Q5Z1J6 nocardia fa
260	61.5	13.3	216	2	Q7V8X4_9PROM	Q7V8X4 prochloroco	333	61	13.2	502	2	Q5DAPE_SCHJA	Q5DAPE schistosoma
261	61.5	13.3	260	2	Q6RNI0_BRAJA	Q6RNI0 bradyrhizob	334	61	13.2	520	2	Q5SHZ3_ARATH	Q5SHZ3 arabidopsis
262	61.5	13.3	262	2	Q9MB91_AGRIP	Q9MB91 agrotis ips	335	61	13.2	542	2	Q5YVG0_NOCFA	Q5YVG0 nocardia fa
263	61.5	13.3	301	2	Q5SKX5_CRYNE	Q5SKX5 cryptococcu	336	61	13.2	568	2	Q61FR3_CABER	Q61FR3 caenorhabdi
264	61.5	13.3	301	2	Q5KAK4_CRYNE	Q5KAK4 cryptococcu	337	61	13.2	631	2	Q6MLY6_BDEBA	Q6MLY6 bdellovibri
265	61.5	13.3	303	2	Q5R491_PONPY	Q5R491 pongo pygma	338	61	13.2	658	2	Q9DDN7_9TELE	Q9DDN7 apteronotus
266	61.5	13.3	320	2	Q6LRF1_PHOPR	Q6LRF1 photobacter	339	61	13.2	653	2	Q73TB8_WYCPA	Q73TB8 mycobacteri
267	61.5	13.3	327	2	Q6MX9_BDEBA	Q6MX9 bdellovibri	340	61	13.2	1305	1	TCGAP_MOUSE	TCGAP mouse
268	61.5	13.3	342	1	ISTA_SYNY3	Q5Z7Y4 synechocyst	341	61	13.2	1526	2	Q5K7V4_CRYNE	Q5K7V4 crytococcu
269	61.5	13.3	347	2	Q6R1Z2_MOUSE	Q6R1Z2 mus musculu	342	61	13.2	1866	2	Q51B7_CRYNE	Q51B7 streptococ
270	61.5	13.3	381	2	Q6R1V9_LACPL	Q6R1V9 lactobacill	343	60.5	13.1	163	2	Q82HN5_STRAW	Q82HN5 streptomyc
271	61.5	13.3	382	2	Q4Q9N5_LEIMA	Q4Q9N5 leishmania	344	60.5	13.1	176	2	Q5GYF6_XANOR	Q5GYF6 xanthomon
272	61.5	13.3	399	2	Q6RNV3_BRAJA	Q6RNV3 bradyrhizob	345	60.5	13.1	210	2	Q9VJPI_DROME	Q9VJPI drosophila
273	61.5	13.3	427	2	Q5WK85_BACSK	Q5WK85 bacillus ci	346	60.5	13.1	210	1	PYRE_BACCI	PYRE_BACCI
274	61.5	13.3	433	2	Q5K1T7_CHLPN	Q5K1T7 chlamydia p	347	60.5	13.1	210	1	PYRE_BACCR	PYRE_BACCR
275	61.5	13.3	433	2	Q9J597_CHLPN	Q9J597 chlamydia p	348	60.5	13.1	210	1	PYRE_BACCR	PYRE_BACCR
276	61.5	13.3	433	2	Q9Z748_CHLPN	Q9Z748 chlamydia p	349	60.5	13.1	210	2	Q4MJ46_BACCE	Q4MJ46 bacille
277	61.5	13.3	434	2	Q736Y4_BACCI	Q736Y4 bacillus ce	350	60.5	13.1	210	1	Q6RXX0_ARATH	Q6RXX0 arabidopsis
278	61.5	13.3	437	2	Q6RPF5_HUMAN	Q6RPF5 homo sapien	351	60.5	13.1	227	2	Q6RXX0_ARATH	Q6RXX0 arabidopsis
279	61.5	13.3	445	2	Q5T133_SALCH	Q5T133 salmone	352	60.5	13.1	253	2	Q6W741_9NEOP	Q6W741 neurospora
280	61.5	13.3	445	2	Q5PKR4_SALPA	Q5PKR4 salmone	353	60.5	13.1	289	2	Q7S921_NEUCR	Q7S921 neurospora
281	61.5	13.3	445	2	Q82ZL3_SALTI	Q82ZL3 salmone	354	60.5	13.1	295	2	Q22885_ARATH	Q22885 arabidopsis
282	61.5	13.3	445	2	Q8ZL09_SALTY	Q8ZL09 salmone	355	60.5	13.1	306	2	Q4NYU9_9BELT	Q4NYU9 anaeromyxob
283	61.5	13.3	458	2	Q6D860_BRWCT	Q6D860 erwina car	356	60.5	13.1	312	2	Q9KXES_BACHD	Q9KXES bacillus ha
284	61.5	13.3	461	2	Q4FPN8_9LITI	Q4FPN8 acortus amer	357	60.5	13.1	319	2	Q4YCE8_PLABE	Q4YCE8 plasmodium
285	61.5	13.3	495	2	Q4SR06_TETNG	Q4SR06 tetracodon n	358	60.5	13.1	326	2	Q97YK6_SULISO	Q97YK6 sulfoblob
286	61.5	13.3	522	2	Q84D05_LISIV	Q84D05 listeria iv	359	60.5	13.1	327	2	Q5XWRO_SOLTU	Q5XWRO solanum tub
287	61.5	13.3	523	2	Q84D04_LISIV	Q84D04 listeria iv	360	60.5	13.1	340	2	Q81LAZ5_ARATH	Q81LAZ5 arabidopsis
288	61.5	13.3	524	1	P60_LISIV	Q81837 listeria iv	361	60.5	13.1	354	2	Q9M9T5_ARATH	Q9M9T5 arabidopsis
289	61.5	13.3	545	2	Q9QEW6_9PARA	Q9QEW6 measles vir	362	60.5	13.1	427	2	Q9A315_CAVCR	Q9A315 callophacter
290	61.5	13.3	549	2	Q9Y3U6_DROME	Q9Y3U6 drosophila	363	60.5	13.1	434	2	Q4MG72_BACCE	Q4MG72 bacillus ce
291	61.5	13.3	566	2	Q73L70_TREDE	Q73L70 treponema d	364	60.5	13.1	434	2	Q63AK9_BACCC	Q63AK9 bacillus ce
292	61.5	13.3	592	2	Q9PVD1_XENLA	Q9PVD1 xenopus lae	365	60.5	13.1	463	2	Q81CL5_BACCR	Q81CL5 bacillus ce
293	61.5	13.3	668	2	Q8BZU9_MOUSE	Q8BZU9 mus musculu	366	60.5	13.1	463	2	Q8D167_YERPE	Q8D167 yersinia pe
294	61.5	13.3	668	2	Q7TMV1_MOUSE	Q7TMV1 mus musculu	367	60.5	13.1	463	2	Q6EDX2_YERPE	Q6EDX2 yersinia ps
295	61.5	13.3	701	2	Q4G019_HUMAN	Q4G019 homo sapien	368	60.5	13.1	463	2	Q8EC25_YERPE	Q8EC25 yersinia pe
296	61.5	13.3	746	2	Q51KR6_MACGR	Q51KR6 magnaporthe	369	60.5	13.1	474	2	Q63187_BURPS	Q63187 burkholderi
297	61.5	13.3	805	2	Q6Z1Z8_BURMA	Q6Z1Z8 burkholderi	370	60.5	13.1	478	2	Q9KX87_DROME	Q9KX87 drosophila
298	61.5	13.3	831	2	Q60XB5_CABER	Q60XB5 caenorhabdi	371	60.5	13.1	484	2	Q6R861_9CAUD	Q6R861 bacterioph
299	61.5	13.3	855	2	Q63TBI_BURPS	Q63TBI burkholderi	372	60.5	13.1	484	2	Q4ZBP3_9VIRU	Q4ZBP3 bacterioph
300	61.5	13.3	977	2	Q96RDU9_HUMAN	Q96RDU9 homo sapien	373	60.5	13.1	516	2	Q4ZDK0_9VIRU	Q4ZDK0 bacterioph
301	61.5	13.3	977	2	Q5VYK9_HUMAN	Q5VYK9 homo sapien	374	60.5	13.1	516	2	Q9M174_ARATH	Q9M174 arabidopsis
302	61.5	13.3	990	2	Q6Q4G3_HUMAN	Q6Q4G3 homo sapien	375	60.5	13.1	547	2	Q4R401_MACFA	Q4R401 macaca fasc
303	61.5	13.3	1145	2	Q8GUE7_9LILI	Q8GUE7 cynodoea n	376	60.5	13.1	560	2	Q5E1A5_AZOSE	Q5E1A5 azarocetes sp
304	61.5	13.3	1222	2	Q5AL53_CANAL	Q5AL53 candida alb	377	60.5	13.1	618	2	Q9GGW9_9POAL	Q9GGW9 carex backi
305	61.5	13.3	1499	2	Q8YK83_ANASP	Q8YK83 anabaena sp	378	60.5	13.1	638	1	KCNK2_RAT	P22462 rattus norv
306	61.5	13.2	100	2	Q6VBE83_PSESY	Q6VBE83 pseudomonas	379	60.5	13.1	658	2	Q7VBR1_PROMM	Q7VBR1 prochloroco
307	61.5	13.2	139	2	Q87HL7_VIBPA	Q87HL7 vibrio para	380	60.5	13.1	726	2	Q4HSU4_CAMUP	Q4HSU4 campylobact
308	61.5	13.2	157	2	Q8DV17_STRMU	Q8DV17 streptococ	381	60.5	13.1	728	1	PURL_CAMUR	PURL CAMUR
309	61.5	13.2	173	2	Q7Q505_ANOGA	Q7Q505 anopheles g	382	60.5	13.1	742	1	Q4H1H9_CAMCO	Q4H1H9 campylobact
310	61.5	13.2	173	2	Q6MY22_SERMA	Q6MY22 serratia ma	383	60.5	13.1	742	2	Q9Q087_9INFA	Q9Q087 influenza a
311	61.5	13.2	180	2	Q811G6_MOUSE	Q811G6 mus musculu	384	60.5	13.1	776	2	Q7NT42_CHRVO	Q7NT42 chromobacte
312	61.5	13.2	187	2	Q5H2G2_XENTR	Q5H2G2 xenopus tro	385	60.5	13.1	917	2	Q7SV17_STPWA	Q7SV17 staphylococ
313	61.5	13.2	238	2	Q5V6G2_HALMA	Q5V6G2 halobacter	386	60.5	13.1	917	2	Q7PFW7_ANOGA	Q7PFW7 anopheles g
314	61.5	13.2	268	2	Q9AB59_CAUCC	Q9AB59 caulobacter	387	60.5	13.1	1038	2	Q4TUT7_AZOV1	Q4TUT7 azotobacter
315	61.5	13.2	272	2	Q8G9V3_ECOLI	Q8G9V3 escherichia	388	60.5	13.1	1155	2	Q51S12_9REOV	Q51S12 avian ortho
316	61.5	13.2	302	2	Q54880_RAT	Q54880 rattus norv	389	60.5	13.1	1285	2	Q51S13_9REOV	Q51S13 avian ortho
317	61.5	13.2	326	2	Q34086_COCER	Q34086 coccyzus er	390	60.5	13.1	1285	2	Q51S14_9REOV	Q51S14 avian ortho
318	61.5	13.2	326	2	Q762D5_MOUSE	Q762D5 mus musculu	391	60.5	13.1	1285	2	Q51S15_9REOV	Q51S15 avian ortho
319	61.5	13.2	338	1	LGT_TREDE	P60974 treponema d	392	60.5	13.1	1285	2	Q51S16_9REOV	Q51S16 avian ortho
320	61.5	13.2	355	2	Q9S592_COTUA	Q9S592 coturnix co	393	60.5	13.1	1285	2	Q51S17_9REOV	Q51S17 avian ortho
321	61.5	13.2	380	2	Q7PG49_ANOGA	Q7PG49 anopheles g	394	60.5	13.1	1285	2	Q51S18_9REOV	Q51S18 avian ortho
322	61.5	13.2	389	2	Q7T197_CHICK	Q7T197 gallus gall	395	60.5	13.1	1285	2	Q51S19_9REOV	Q51S19 avian ortho
323	61.5	13.2	395	2	Q988F9_RHILLO	Q988F9 rhizobium 1	396	60.5	13.1	1285	2		

397	60.5	13.1	1285	2	08JUV1_9REOV	08JUV1 avian recvi	470	59.5	12.9	579	2	05GTF9_WOLTR	05GTF9 wolbachia s
398	60.5	13.1	1319	2	05AYC8_EMENT	05AYC8 aspergillus	471	59.5	12.9	579	2	073166_WOLPM	073166 wolbachia p
399	60.5	13.1	1748	2	09HGZ5_ASPOR	09HGZ5 aspergillus	472	59.5	12.9	624	2	053X46_CRYNE	053X46 cryptococcus
400	60	13.0	71	1	VITB1_XENIA	P1010 xenopus lae	473	59.5	12.9	624	2	05KMT6_CRYNE	05KMT6 cryptococcus
401	60	13.0	165	2	08BEP3_OCEIH	08BEP3 oceanobacti	474	59.5	12.9	636	2	04ZRP6_PSESY	04ZRP6 pseudomonas
402	60	13.0	218	2	06LTC3_PHOPR	06LTC3 photobacter	475	59.5	12.9	636	2	087ZAB_PSESY	087ZAB pseudomonas
403	60	13.0	249	2	08MM93_BRARE	08MM93 brachydanio	476	59.5	12.9	677	2	098TW3_XENIA	098TW3 xenopus lae
404	60	13.0	269	2	08YXA0_ANAPSE	08YXA0 anabaena sp	477	59.5	12.9	715	2	08PSH8_METWA	08PSH8 methanobact
405	60	13.0	275	2	09VLF6_DROME	09VLF6 drosophila	478	59.5	12.9	735	2	05E3S0_VIBFL	05E3S0 vibrio fusc
406	60	13.0	288	2	08B1Q0_PSEPK	08B1Q0 pseudomonas	479	59.5	12.9	778	2	04RVZ3_TETNG	04RVZ3 tetradodon n
407	60	13.0	316	2	09YVNI_DROME	09YVNI drosophila	480	59.5	12.9	841	2	08H1O5_ARATH	08H1O5 arabidopsis
408	60	13.0	324	2	0986J3_RHIO	0986J3 rhizobium l	481	59.5	12.9	841	2	08RWY4_ARATH	08RWY4 arabidopsis
409	60	13.0	325	2	07XMP8_ORYSA	07XMP8 oryza sativ	482	59.5	12.9	847	2	09SGW2_ARATH	09SGW2 arabidopsis
410	60	13.0	341	1	PAX9_HUMAN	P55771 homo sapien	483	59.5	12.9	894	2	08T043_DROME	08T043 drosophila
411	60	13.0	342	1	PAX9_MOUSE	P47242 mus musculu	484	59.5	12.9	1037	2	09VZS3_DROME	09VZS3 drosophila
412	60	13.0	342	2	08BSB1_MOUSE	08BSB1 mus musculu	485	59.5	12.9	1048	2	04NQ40_9DELT	04NQ40 9delu
413	60	13.0	352	2	05DMS5_KARMI	05DMS5 karlodinim	486	59.5	12.9	1138	2	012371_VITUR	012371 vitru
414	60	13.0	365	2	069135_9GAMA	069135 human heape	487	59.5	12.9	1800	2	081RF5_DICDI	081RF5 dictyostei
415	60	13.0	369	2	06D4F3_ERWCT	06D4F3 erwinta car	488	59.5	12.9	1800	2	081RF5_DICDI	081RF5 dictyostei
416	60	13.0	378	2	08AZK9_9GAMA	08AZK9 human heape	489	59.5	12.8	119	2	054PVL_DICDI	054PVL dictyostei
417	60	13.0	412	2	0913M4_PSEAE	0913M4 pseudomonas	490	59.5	12.8	130	2	09GMZ2_PIG	09GMZ2 pig
418	60	13.0	497	1	LMP2_EBV	P13285 Epstein-Bar	491	59.5	12.8	149	2	08XBD8_ECOS7	08XBD8 ecocost
419	60	13.0	497	2	0777H4_9GAMA	0777H4 human herpe	492	59.5	12.8	150	2	08HUG2_LACPL	08HUG2 lactobacill
420	60	13.0	502	2	09BGM9_9GAMA	09BGM9 human herpe	493	59.5	12.8	155	2	06D7R0_ERMCT	06D7R0 erwinta car
421	60	13.0	518	2	09XEO1_STRVG	09XEO1 streptomyce	494	59.5	12.8	167	2	092317_MOUSE	092317 mus musculu
422	60	13.0	519	2	082LO9_STRAW	082LO9 streptomyce	495	59.5	12.8	167	2	08W9B3_VOMUR	08W9B3 vomibact ur
423	60	13.0	524	2	071198_CHICK	071198 gallus gall	496	59.5	12.8	169	2	0744R5_MYCPA	0744R5 mycobacteri
424	60	13.0	525	2	083J01_SHIFL	083J01 shigella fl	497	59.5	12.8	175	2	079713_FALPE	079713 falco peregr
425	60	13.0	538	1	Y1EC_ECOLI	P26218 escherichia	498	59.5	12.8	177	2	092AM4_LISIN	092AM4 listeria in
426	60	13.0	541	2	05KMT3_CRYNE	05KMT3 cryptococcu	499	59.5	12.8	189	2	06X910_SULTS	06X910 sulfatobus
427	60	13.0	565	2	08VD01_MOUSE	08VD01 mus musculu	500	59.5	12.8	189	2	06X911_SULTS	06X911 sulfatobus
428	60	13.0	580	2	071195_CHICK	071195 gallus gall	501	59.5	12.8	189	2	06X917_SULTS	06X917 sulfatobus
429	60	13.0	605	2	07NHD8_GLOVI	07NHD8 gloobacter	502	59.5	12.8	199	2	06X9M0_SULTS	06X9M0 sulfatobus
430	60	13.0	611	2	08BYF6_MOUSE	08BYF6 m mus muscu	503	59.5	12.8	215	1	YCHE_ECOLI	P57373 escherichia
431	60	13.0	616	2	09Y1A2_TRYBB	09Y1A2 trypanosoma	504	59.5	12.8	215	2	08FHX1_ECOLI	08FHX1 escherichia
432	60	13.0	616	2	0581Z5_9RRYP	0581Z5 trypanosoma	505	59.5	12.8	215	2	083RNI_SHIFL	083RNI shigella fl
433	60	13.0	756	2	055Z68_CRYNE	055Z68 cryptococcu	506	59.5	12.8	215	2	08XDAS_ECOS7	08XDAS escherichia
434	60	13.0	793	2	094BY0_ARATH	094BY0 arabidopsis	507	59.5	12.8	284	2	0594H3_9SPHN	0594H3 agrobacterci
435	60	13.0	819	1	US6NL_MOUSE	080XC3 mus musculu	508	59.5	12.8	293	1	PUR7_BORBR	0594H3 bordetella
436	60	13.0	876	2	Q4ITTS_AZOVI	Q4ITTS azotobacter	509	59.5	12.8	293	1	PUR7_BORBR	0594H3 bordetella
437	60	13.0	1056	2	Q4UWV2_XANCP	Q4UWV2 xanthomonas	510	59.5	12.8	293	1	PUR7_BORBR	0594H3 bordetella
438	60	13.0	1056	2	Q8B875_XANCP	Q8B875 xanthomonas	511	59.5	12.8	310	2	09A410_CAUCR	09A410 caulobacter
439	60	13.0	1157	2	Q6BHA0_DEBHA	Q6BHA0 debaryomyce	512	59.5	12.8	326	2	0577P4_BRUBA	0577P4 bruceella ab
440	60	13.0	3187	2	Q4S6R6_TETNG	Q4S6R6 tetradodon n	513	59.5	12.8	326	2	08FWG7_BRUBA	08FWG7 bruceella ab
441	60	13.0	5217	1	HTS1_COCCA	001886 cochllobolu	514	59.5	12.8	326	2	08BIV7_BRUME	08BIV7 bruceella me
442	59.5	12.9	209	2	05KMN0_CRYNE	05KMN0 cryptococcu	515	59.5	12.8	345	1	ARGC_BACHK	0635F0 bacillus h
443	59.5	12.9	214	2	07N4S9_PHOIL	07N4S9 photorhabdu	516	59.5	12.8	345	2	0635F0_BACZ	0635F0 bacillus ce
444	59.5	12.9	216	2	09GJG8_SALTR	09GJG8 salmo trutt	517	59.5	12.8	350	2	07MOY1_WOLSU	07MOY1 wolbachia s
445	59.5	12.9	216	2	09GJG8_SALTR	09GJG8 salmo trutt	518	59.5	12.8	356	2	07XUY8_ORYSA	07XUY8 oryza sativ
446	59.5	12.9	216	2	09GJH0_SALTR	09GJH0 salmo trutt	519	59.5	12.8	369	2	07QZG4_GIALA	07QZG4 giardia lam
447	59.5	12.9	217	2	09GJH3_SALTR	09GJH3 salmo trutt	520	59.5	12.8	370	2	098F86_RHIL0	098F86 rhizobium l
448	59.5	12.9	217	2	09GJH4_SALTR	09GJH4 salmo trutt	521	59.5	12.8	381	2	05OWF6_ENTHI	05OWF6 entamoeba h
449	59.5	12.9	217	2	09GJH6_SALTR	09GJH6 salmo trutt	522	59.5	12.8	419	2	097VB7_SULTS0	097VB7 sulfatobus
450	59.5	12.9	223	2	09GJH7_SALTR	09GJH7 salmo trutt	523	59.5	12.8	420	2	0926F0_RHIME	0926F0 rhizobium m
451	59.5	12.9	223	2	06PER5_MOUSE	06PER5 mus musculu	524	59.5	12.8	447	2	0836T8_ENTRA	0836T8 enterococcu
452	59.5	12.9	228	2	Q4RUQ4_TETNG	Q4RUQ4 tetradodon n	525	59.5	12.8	447	2	0605T5_METCA	0605T5 methylococc
453	59.5	12.9	260	2	086A07_DICDI	086A07 dictyostei	526	59.5	12.8	448	2	07NZNO_CHRVO	07NZNO chromobacte
454	59.5	12.9	267	2	09CG47_IACLA	09CG47 lactococcus	527	59.5	12.8	463	2	08JHG2_BRARE	08JHG2 brachydanio
455	59.5	12.9	298	2	09KXR2_VIBCH	09KXR2 vibrio chol	528	59.5	12.8	463	2	06PCJ5_BRARE	06PCJ5 brachydanio
456	59.5	12.9	341	2	0880A3_PSESM	0880A3 pseudomonas	529	59.5	12.8	479	1	NUON2_RHIME	066911 pseudomonas
457	59.5	12.9	342	2	09G5Z0_9SAUR	09G5Z0 pseudocariot	530	59.5	12.8	526	2	06X1D5_9RHAH	06X1D5 aravan vitu
458	59.5	12.9	346	2	08XKMO_CLOPE	08XKMO clostridium	531	59.5	12.8	552	2	Q4IBY1_GIBZE	Q4IBY1 gibberella
459	59.5	12.9	358	2	09YMM0_NIPLD	09YMM0 lymantria d	532	59.5	12.8	557	2	05R7Q0_PONPY	05R7Q0 pongo pygma
460	59.5	12.9	384	2	072DS9_DESVH	072DS9 desulfovibr	533	59.5	12.8	558	2	092CG0_LISIN	092CG0 listeria in
461	59.5	12.9	385	2	04SSP1_TETNG	04SSP1 tetradodon n	534	59.5	12.8	575	2	09OUU4_9MPSI	09OUU4 ratius sp.
462	59.5	12.9	396	2	09UJH3_CAEEL	09UJH3 caenorhadi	535	59.5	12.8	579	2	06U666_KLEPN	06U666 klebsiella
463	59.5	12.9	397	2	08XSK3_RALSO	08XSK3 ralfsonia s	536	59.5	12.8	598	2	Q4SUK0_TETNG	Q4SUK0 tetradodon n
464	59.5	12.9	426	2	06FJK9_CANGA	06FJK9 candida gla	537	59.5	12.8	611	2	08MNO3_PIG	08MNO3 sus scrofa
465	59.5	12.9	431	2	Q7XTD3_ORYSA	Q7XTD3 oryza sativ	538	59.5	12.8	623	2	053W46_THET8	053W46 thermus the
466	59.5	12.9	526	2	Q7VIO6_HEIHP	Q7VIO6 helicobacte	539	59.5	12.8	653	2	05REB6_PONPY	05REB6 pongo pygma
467	59.5	12.9	527	1	TH11_TRYBB	066221 trypanosoma	540	59.5	12.8	654	1	KCNM4_MOUSE	061443 mus musculu
468	59.5	12.9	527	1	Q26T65_9RRYP	Q26T65 trypanosoma	541	59.5	12.8	654	1	KCNM4_MOUSE	061443 mus musculu
469	59.5	12.9	528	1	TH12_TRYBB	Q09037 trypanosoma	542	59.5	12.8	654	2	Q8CBF8_MOUSE	Q8CBF8 mus musculu

543	59	12.8	655	1	KCN4A_RAT	P15385	rattus	novi	616	58.5	12.7	426	2	069513	MYCLE	069513	mycobacteri
544	59	12.8	660	1	KCN4A_BOVIN	005037	bos	taurus	617	58.5	12.7	463	2	09CB73	MYCLE	09CB73	mycobacteri
545	59	12.8	660	2	084MG6_ORYSA	084MG6	oryza	sativ	618	58.5	12.7	471	2	04S1G4	TETNG	04S1G4	tetrarodon n
546	59	12.8	661	2	09GLF1_BOVIN	09GLF1	bos	taurus	619	58.5	12.7	482	2	097CF4	THEVO	097CF4	thermoplasm
547	59	12.8	662	2	090W36_COLLI	090W36	columbia	liv	620	58.5	12.7	499	2	04NDZ1	9MICC	04NDZ1	9microbact
548	59	12.8	662	2	09YXG8_CHALL	09YXG8	gallus	gall	621	58.5	12.7	509	2	08NSN5	9TRYP	08NSN5	trypanosoma
549	59	12.8	663	2	061VQ2_CAEBR	061VQ2	caenorhabd		622	58.5	12.7	516	2	084DM1	LISSE	084DM1	listeria se
550	59	12.8	697	2	08UG57_XENLA	08UG57	xenopus	lae	623	58.5	12.7	516	2	084DU3	LISSE	084DU3	listeria se
551	59	12.8	700	2	05R4E7_PONPY	05R4E7	pongo	pygma	624	58.5	12.7	557	2	08VZE2	ARATH	08VZE2	arabidopsis
552	59	12.8	721	2	080X33_MOUSE	080X33	mus	musculu	625	58.5	12.7	565	2	0833DE	COXBU	0833DE	coxiella bu
553	59	12.8	782	2	06LKY8_PHOPE	06LKY8	photobacter		626	58.5	12.7	587	2	091A25	ONCMY	091A25	oncorhynch
554	59	12.8	787	2	05SMW7_ORYSA	05SMW7	oryza	sativ	627	58.5	12.7	633	2	04HWN9	GIBZE	04HWN9	gibberella
555	59	12.8	816	2	098SV4_ICTPU	098SV4	icetallurus	p	628	58.5	12.7	639	2	06VTW8	INPCD	06VTW8	infectio
556	59	12.8	855	2	07NBTO_MYCGA	07NBTO	mycoplasma		629	58.5	12.7	682	2	05CN79	CRPHO	05CN79	cryptospori
557	59	12.8	857	1	KCNB1_MOUSE	003117	mus	musculu	630	58.5	12.7	683	2	058QF6	WHEAT	058QF6	wheat
558	59	12.8	857	1	KCNB1_RAT	P15387	rattus	novi	631	58.5	12.7	716	2	058QF6	WHEAT	058QF6	wheat
559	59	12.8	857	2	08KOD1_MOUSE	08KOD1	mus	musculu	632	58.5	12.7	716	2	053UC8	WHEAT	053UC8	wheat
560	59	12.8	858	1	KCNB1_HUMAN	014721	homo	sapien	633	58.5	12.7	719	2	089ZNE	BACTN	089ZNE	bacteroides
561	59	12.8	858	1	KCNB1_PIG	018668	sus	scrofa	634	58.5	12.7	726	2	08HTN2	9MAGN	08HTN2	9mag
562	59	12.8	858	1	KCNB1_RABIT	09m1592	xenopus	lae	635	58.5	12.7	876	2	05FAU3	NEIG1	05FAU3	neisseria g
563	59	12.8	898	2	091592_XENLA	091592	xenopus	lae	636	58.5	12.7	878	2	05FAU3	NEIG1	05FAU3	neisseria g
564	59	12.8	907	1	KCNB2_RAT	063089	rattus	novi	637	58.5	12.7	1048	2	06EMD9	ECOLI	06EMD9	escherichia
565	59	12.8	911	1	KCNB2_HUMAN	092953	homo	sapien	638	58.5	12.7	1048	2	0605N9	KLEPN	0605N9	klebsiella
566	59	12.8	911	1	KCNB2_RABIT	095111	oryctolagus		639	58.5	12.7	1095	2	09C7H5	ARATH	09C7H5	arabidopsis
567	59	12.8	911	2	07Z7D0_HUMAN	07Z7D0	homo	sapien	640	58.5	12.7	1105	2	05F3N7	CHICK	05F3N7	chick
568	59	12.8	912	2	04ZHA6_BOVIN	04ZHA6	bos	taurus	641	58.5	12.7	1189	2	044415	9RHIZ	044415	9rhiz
569	59	12.8	936	2	06GNN5_XENLA	06GNN5	xenopus	lae	642	58.5	12.7	1346	2	05XGR8	MAGCR	05XGR8	mag
570	59	12.8	971	2	05AKB1_EMBNI	05AKB1	aspergillus		643	58.5	12.7	1720	2	04FXS8	LEIMA	04FXS8	leishmania
571	59	12.8	1078	2	041S20_AZCVI	041S20	azotobacter		644	58.5	12.7	1817	2	07SZFE	XENLA	07SZFE	xenopus lae
572	59	12.8	1211	2	057WZ8_9TRYP	057WZ8	trypanosoma		645	58.5	12.7	2473	2	0951C7	9MAMN	0951C7	tachylosu
573	59	12.8	1463	2	04P3P5_USTMA	04P3P5	ustilago	ma	646	58.5	12.7	2710	2	0873G9	CABEL	0873G9	cabel
574	58.5	12.7	133	2	08DA24_VIBU	08DA24	vibrio	vuln	647	58.5	12.7	2712	2	001808	CABEL	001808	caenorhabd
575	58.5	12.7	153	2	07MK55_VIBVY	07MK55	vibrio	vuln	648	58.5	12.7	5359	2	05VKR4	SACCR	05VKR4	saccharopol
576	58.5	12.7	169	2	06MLM7_BDEBA	06MLM7	bdellovibri		649	58.5	12.7	6193	2	08KSD0	STRCP	08KSD0	streptomyce
577	58.5	12.7	182	2	0916C9_PSEBA	0916C9	pseudomonas		650	58	12.6	96	2	083EB8	COXBU	083EB8	coxiella bu
578	58.5	12.7	196	2	07QBB9_ANOGA	07QBB9	anopheles	g	651	58	12.6	104	2	024949	FASHE	024949	faecicola he
579	58.5	12.7	196	1	CLPP_HEILP	07V9E9	helicobacter		652	58	12.6	114	1	YDGD	BACBU	YDGD	bacillus bu
580	58.5	12.7	200	2	04TTB7_CABEL	04TTB7	caenorhabd		653	58	12.6	120	2	04U5Z8	ACZCVI	04U5Z8	azotobacter
581	58.5	12.7	200	2	0852L5_ORYSA	0852L5	oryza	sativ	654	58	12.6	175	2	05WAS8	BACSC	05WAS8	bacillus cl
582	58.5	12.7	217	2	096XK6_SULTO	096XK6	sulfolobus		655	58	12.6	177	2	095UM4	LISIN	095UM4	listeria in
583	58.5	12.7	221	2	04SQX2_TETNG	04SQX2	tetrarodon	n	656	58	12.6	185	2	05PU65	SALPA	05PU65	salmone
584	58.5	12.7	222	2	07N7R7_PHOIL	07N7R7	photorhabd		657	58	12.6	185	2	082152	SALTI	082152	salmone
585	58.5	12.7	238	2	04SDB4_TETNG	04SDB4	tetrarodon	n	658	58	12.6	185	2	082K73	SALTY	082K73	salmone
586	58.5	12.7	239	2	0661B5_BRABE	0661B5	brachydanio		659	58	12.6	196	2	09RYZ1	DEIRA	09RYZ1	deinococcus
587	58.5	12.7	260	1	NRPN_HUMAN	060259	homo	sapien	660	58	12.6	215	2	05TNR2	SALCH	05TNR2	salmone
588	58.5	12.7	260	2	081W69_HUMAN	081W69	homo	sapien	661	58	12.6	215	2	05PCV5	SALPA	05PCV5	salmone
589	58.5	12.7	265	2	088YT6_LACPL	088YT6	lactobacill		662	58	12.6	215	2	07CQF4	SALTY	07CQF4	salty
590	58.5	12.7	299	2	0603A7_MERCA	0603A7	methylcoccc		663	58	12.6	215	2	08XFE2	SALTI	08XFE2	salmone
591	58.5	12.7	299	2	07WOP0_BORBE	07WOP0	borderella		664	58	12.6	232	2	05E000	VIBF1	05E000	vibrio fibc
592	58.5	12.7	299	2	07W3G6_BORBA	07W3G6	borderella		665	58	12.6	257	1	DPHB	METJA	DPHB	met
593	58.5	12.7	299	2	07WET6_BORBR	07WET6	borderella		666	58	12.6	263	2	09FPB4	ORYSA	09FPB4	oryza sativ
594	58.5	12.7	299	2	07WUJ4_CHRVO	07WUJ4	chromobacter		667	58	12.6	277	1	RATP	PEDPE	RATP	ped
595	58.5	12.7	303	2	05XYK9_ARATH	05XYK9	arabidopsis		668	58	12.6	314	2	061K08	DROME	061K08	drosophila
596	58.5	12.7	321	1	TILS_BORPE	07V9X2	arabidopsis		669	58	12.6	325	2	09ELT9	9VIRU	09ELT9	rice grassy
597	58.5	12.7	328	2	06LEX6_PLAF7	06LEX6	plasmodium		670	58	12.6	331	2	065F35	BACLD	065F35	ba
598	58.5	12.7	336	2	082BR5_STRAM	082BR5	streptomyce		671	58	12.6	333	2	08N7W6	HUMAN	08N7W6	homo sapien
599	58.5	12.7	340	2	08R7B2_THETN	08R7B2	thermosaer		672	58	12.6	344	2	04V1K5	BACCC	04V1K5	ba
600	58.5	12.7	344	2	04NG06_9MICC	04NG06	athrobacter		673	58	12.6	345	2	06AXV5	RAT	06AXV5	ratt
601	58.5	12.7	352	2	05BCR9_CANFA	05BCR9	canis	famil	674	58	12.6	349	2	07MGC8	VIBVY	07MGC8	vibrio vuln
602	58.5	12.7	352	2	05SKV8_CANFA	05SKV8	canis	famil	675	58	12.6	354	2	095HB3	ANAPL	095HB3	ana
603	58.5	12.7	359	2	05LSF2_CHLAB	05LSF2	chlamydomo		676	58	12.6	368	2	023311	CABEL	023311	caenorhabd
604	58.5	12.7	366	2	0898R9_BRABA	0898R9	bradyrhizob		677	58	12.6	376	2	0926X3	LISIN	0926X3	listeria in
605	58.5	12.7	372	2	08SGX1_9SAUR	08SGX1	pareas	macu	678	58	12.6	383	2	081BN5	BACCR	081BN5	ba
606	58.5	12.7	383	1	FADBE_ARATH	FADBE	arabidopsis		679	58	12.6	395	2	07PSF3	ANOGA	07PSF3	an
607	58.5	12.7	383	2	081FZ8_ARATH	081FZ8	arabidopsis		680	58	12.6	398	1	SELI	MOUSE	SELI	mouse
608	58.5	12.7	384	2	08UAR7_AGRYS	08UAR7	agrobacteri		681	58	12.6	403	2	09KPH1	VIBCH	09KPH1	vibrio chol
609	58.5	12.7	385	2	06ZLU9_AGRYS	06ZLU9	oryza	sativ	682	58	12.6	408	2	05F7W0	NEIG1	05F7W0	neisseria g
610	58.5	12.7	392	2	07CS44_AGRYS	07CS44	agrobacteri		683	58	12.6	409	2	04MX56	BACCC	04MX56	ba
611	58.5	12.7	392	2	06C9T8_YARUT	06C9T8	yarrowia	ll	684	58	12.6	411	2	07YOP7	OCHPR	07YOP7	och
612	58.5	12.7	400	1	EFTU_HERAV	P42477	hepeliophilu		685	58	12.6	440	2	04MSY3	BACCC	04MSY3	ba
613	58.5	12.7	409	2	08DBZ6_VIBVU	08DBZ6	vibrio	vuln	686	58	12.6	440	2	06HKY9	BACCH	06HKY9	ba
614	58.5	12.7	411	2	09RU03_DEIRA	09RU03	deinococcus		687	58	12.6	440	2	081FL1	BACCR	081FL1	ba
615	58.5	12.7	425	1	YOSH_SCHPO	09P712	schizosacch		688	58	12.6	440	2				

689	58	12.6	440	2	Q73A54_BACCI	Q73A64_bacillus ce	762	57.5	12.5	388	2	Q54466_STRMY	Q54466 streptomyc
690	58	12.6	440	2	Q63D66_BACCA	Q63D66 bacillus ce	763	57.5	12.5	401	2	Q87427_PODAN	Q87427 podopora a
691	58	12.6	440	2	Q81S04_BACAN	Q81S04 bacillus an	764	57.5	12.5	402	2	Q72702_HUMAN	Q72702 homo sapien
692	58	12.6	444	2	Q4SMG6_TETNG	Q4SMG6 tetrading	765	57.5	12.5	426	2	Q57137_9BETA	Q57137 human herpe
693	58	12.6	448	2	Q84DP2_LISMO	Q84DP2 listeria mo	766	57.5	12.5	433	2	Q4H838_9DEIO	Q4H838 deinococcus
694	58	12.6	457	2	Q4KJF7_PSEPF	Q4KJF7 pseudomonas	767	57.5	12.5	441	2	Q60N14_CAEBR	Q60N14 ceenorhabdi
695	58	12.6	461	2	Q8ZR07_SALTY	Q8ZR07 salmonella	768	57.5	12.5	446	2	Q6H703_ORYSA	Q6H703 oryza sativ
696	58	12.6	462	2	Q8RYH5_DEIRA	Q8RYH5 deinococcus	769	57.5	12.5	448	2	Q6NB17_RHOFA	Q6NB17 rhodopseudo
697	58	12.6	486	2	Q6DBW3_BRARE	Q6DBW3 brachydanio	770	57.5	12.5	453	2	Q7ZVN2_BRARE	Q7ZVN2 brachydanio
698	58	12.6	487	2	Q4T7M0_TETNG	Q4T7M0 tetrading	771	57.5	12.5	461	2	Q5PM91_SALPA	Q5PM91 salmonella
699	58	12.6	511	2	Q74CB3_GEOSL	Q74CB3 geobacter s	772	57.5	12.5	461	2	Q8Z815_SALTI	Q8Z815 salmonella
700	58	12.6	541	2	Q9Y111_LOOMI	Q9Y111 locusta mig	773	57.5	12.5	461	2	Q916E1_PSEAR	Q916E1 pseudomonas
701	58	12.6	549	2	Q8GGR2_STRAZ	Q8GGR2 streptomyc	774	57.5	12.5	461	2	Q6SQY2_MANSN	Q6SQY2 manheimia
702	58	12.6	552	2	Q4J3Z2_AZOVI	Q4J3Z2 azotobacter	775	57.5	12.5	502	2	Q5V1D8_HALMA	Q5V1D8 haloarcula
703	58	12.6	553	2	Q942J6_ORYSA	Q942J6 oryza sativ	776	57.5	12.5	507	2	Q5PPFS_RAT	Q5PPFS rattus norv
704	58	12.6	614	2	Q7UVX4_RHOBA	Q7UVX4 rhodospirill	777	57.5	12.5	517	2	Q8BVA5_MYCPE	Q8BVA5 mycoplasma
705	58	12.6	629	2	Q86146_CAMJE	Q86146 campylobact	778	57.5	12.5	523	2	Q916Z6_PSEAE	Q916Z6 pseudomonas
706	58	12.6	674	2	Q8BHZ1_XANAC	Q8BHZ1 xanthomonas	779	57.5	12.5	528	1	KCNJ13_MOUSE	P16390 mus musculu
707	58	12.6	675	2	Q5H2Z6_XANOR	Q5H2Z6 xanthomonas	780	57.5	12.5	531	2	Q8ERGI_OCEBH	Q8ERGI oceanobacil
708	58	12.6	676	2	Q8XQ93_RALSO	Q8XQ93 ralstonia s	781	57.5	12.5	541	2	Q4SEY1_TETNG	Q4SEY1 tetrading
709	58	12.6	681	1	GAZL1_HUMAN	Q93501 homo sapien	782	57.5	12.5	574	2	Q8XQ27_RALSO	Q8XQ27 ralstonia s
710	58	12.6	682	1	Q4HUI4_GIBZE	Q4HUI4 glibberella	783	57.5	12.5	581	2	Q6BK68_DEBHA	Q6BK68 debaryomyce
711	58	12.6	695	2	Q4HLX6_CAMLA	Q4HLX6 campylobact	784	57.5	12.5	594	2	Q98PX5_MYCPV	Q98PX5 mycoplasma
712	58	12.6	743	2	Q6FUV9_CANGA	Q6FUV9 candida gla	785	57.5	12.5	603	2	Q4P4K6_USTWA	Q4P4K6 ustula
713	58	12.6	758	2	Q9VQW0_DROME	Q9VQW0 drosophila	786	57.5	12.5	636	2	Q86486_PPARA	Q86486 pparc
714	58	12.6	767	2	Q51CVO_DENTH	Q51CVO entamoeba h	787	57.5	12.5	636	2	Q8K244_MOUSE	Q8K244 mus musculu
715	58	12.6	778	2	Q60ZP1_CAEBR	Q60ZP1 caenorhabdi	788	57.5	12.5	662	1	HEPA_HHV6Z	P52451 human herpe
716	58	12.6	876	2	Q91593_XENLA	Q91593 xenopus lae	789	57.5	12.5	662	2	Q9WT01_9BETA	Q9WT01 human herpe
717	58	12.6	978	2	Q5BBD3_EMENT	Q5BBD3 aspergillus	790	57.5	12.5	668	2	Q4UKH5_XANCP	Q4UKH5 xanthomonas
718	58	12.6	1006	2	Q4NI49_9MICC	Q4NI49 aspergillus	791	57.5	12.5	668	2	Q8P6N7_XANCP	Q8P6N7 xanthomonas
719	58	12.6	1018	2	Q6ALX0_DESPS	Q6ALX0 desulfotale	792	57.5	12.5	670	2	Q9BNA4_9MAGN	Q9BNA4 buxus citri
720	58	12.6	1051	2	Q5S9V4_EMENT	Q5S9V4 aspergillus	793	57.5	12.5	671	2	Q5AKV5_CANAL	Q5AKV5 candida alb
721	58	12.6	1056	2	Q7S8Q2_NEUCR	Q7S8Q2 neurospora	794	57.5	12.5	692	2	Q9BAR1_9MAGN	Q9BAR1 buxus glome
722	58	12.6	1056	2	Q8BJN1_XANAC	Q8BJN1 xanthomonas	795	57.5	12.5	745	1	PURL_HELHP	Q519G2 entamoeba h
723	58	12.6	1109	2	Q7JRS2_DROME	Q7JRS2 drosophila	796	57.5	12.5	750	2	Q519G2_ENTHI	Q519G2 ceenorhabdi
724	58	12.6	1135	2	Q9V7B8_DROME	Q9V7B8 drosophila	797	57.5	12.5	771	2	Q617U6_CAEBR	Q617U6 ceenorhabdi
725	58	12.6	1149	2	Q7KUP4_DROME	Q7KUP4 drosophila	798	57.5	12.5	772	2	Q75JF4_DICDI	Q75JF4 dictyosteli
726	58	12.6	1821	2	Q7PQL1_ANOGA	Q7PQL1 anopheles g	799	57.5	12.5	794	2	Q6P440_XENLA	Q6P440 xenopus lae
727	58	12.6	1905	2	Q9XTE6_PLABE	Q9XTE6 plasmodium	800	57.5	12.5	822	2	Q81QW2_DROME	Q81QW2 drosophila
728	58	12.6	2576	2	Q4UFV5_BRARE	Q4UFV5 brachydanio	801	57.5	12.5	857	1	OPGH_PSEPK	Q86D40 pseudomonas
729	58	12.6	4836	2	Q4U2R1_MOUSE	Q4U2R1 mus musculu	802	57.5	12.5	865	2	Q61UJ8_CAEBR	Q61UJ8 ceenorhabdi
730	58	12.6	4836	2	Q88473_MOUSE	Q88473 mus musculu	803	57.5	12.5	882	2	Q8MOK2_DROME	Q8MOK2 drosophila
731	57.5	12.5	71	1	VITB2_XENLA	P19011 xenopus lae	804	57.5	12.5	907	2	Q8VY10_ARATH	Q8VY10 arabidopsis
732	57.5	12.5	84	2	Q8TFE5_DROPS	Q8TFE5 drosophila	805	57.5	12.5	1012	2	Q8XUM5_RALSO	Q8XUM5 ralstonia s
733	57.5	12.5	128	2	Q9NG96_MAMBR	Q9NG96 mamestra br	806	57.5	12.5	1071	2	Q993JF2_9GAMA	Q993JF2 callitrichi
734	57.5	12.5	129	2	Q4K8V9_PSEFS	Q4K8V9 pseudomonas	807	57.5	12.5	1625	2	Q6MWD4_NEUCR	Q6MWD4 neurospora
735	57.5	12.5	139	2	Q8Z6V7_SALTI	Q8Z6V7 salmonella	808	57.5	12.5	1681	2	Q4SVT8_TETNG	Q4SVT8 tetrading
736	57.5	12.5	144	2	Q5YXC3_NOCFA	Q5YXC3 nocardia fa	809	57.5	12.5	1696	2	Q4NOK7_THEPA	Q4NOK7 thellesia p
737	57.5	12.5	144	2	Q9BFR0_RAT	Q9BFR0 rattus norv	810	57.5	12.5	1751	2	Q5VY95_STRYP	Q5VY95 streptococ
738	57.5	12.5	146	2	Q5LS51_SILPO	Q5LS51 silicibacte	811	57.5	12.5	1902	1	P2P_LACPA	Q60ZNS caebrr
739	57.5	12.5	153	2	Q8K0V1_MOUSE	Q8K0V1 mus musculu	812	57.5	12.5	2235	1	CHD7_HUMAN	Q60ZNS caebrr
740	57.5	12.5	173	2	Q8SCX0_9TELE	Q8SCX0 salangichth	813	57.5	12.5	2322	2	Q4N1Z7_THEPA	Q4N1Z7 thellesia p
741	57.5	12.5	184	2	Q5U4U5_XENLA	Q5U4U5 xenopus lae	814	57.5	12.5	3300	2	Q60ZNS_CAEBR	Q60ZNS caebrr
742	57.5	12.5	194	2	Q5BINA_BOVIN	Q5BINA bos taurus	815	57	12.4	105	2	Q4FTI0_9GAMW	Q4FTI0 psychrobact
743	57.5	12.5	224	1	CLBPI1_SYNDX	Q7NA36 synecococc	816	57	12.4	148	2	Q8LGH9_ARATH	Q8LGH9 arabidopsis
744	57.5	12.5	242	2	Q83TJ3_SALTI	Q83TJ3 salmonella	817	57	12.4	148	2	Q9ZV24_ARATH	Q9ZV24 arabidopsis
745	57.5	12.5	255	2	Q7XQ06_ORYSA	Q7XQ06 oryza sativ	818	57	12.4	152	2	Q8ES95_STRAJ	Q8ES95 streptococ
746	57.5	12.5	292	2	Q6FUC0_CANGA	Q6FUC0 candida gla	819	57	12.4	158	2	Q6FSW5_CANGA	Q6FSW5 candida gla
747	57.5	12.5	307	2	Q467Z0_ECOLI	Q467Z0 escherichia	820	57	12.4	166	2	Q61UJ1_DROME	Q61UJ1 drosophila
748	57.5	12.5	313	2	Q7NMF7_CHRVO	Q7NMF7 chromobacte	821	57	12.4	171	2	Q5COK4_SCHJA	Q5COK4 schistosoma
749	57.5	12.5	323	2	Q9JH09_STRAC	Q9JH09 streptomyc	822	57	12.4	177	2	Q5IKR5_SILPO	Q5IKR5 silicibacte
750	57.5	12.5	324	2	Q9S248_STRCO	Q9S248 streptomyc	823	57	12.4	184	2	Q8LE27_ARATH	Q8LE27 arabidopsis
751	57.5	12.5	337	2	Q817B2_FASHE	Q817B2 fasciola he	824	57	12.4	184	2	Q4TMQ7_GSPHN	Q4TMQ7 erythrobact
752	57.5	12.5	342	1	ISIA_SYNP2	P31157 synecococc	825	57	12.4	185	1	ADML_RAT	P3145 rattus norv
753	57.5	12.5	353	2	Q9LR55_ARATH	Q9LR55 arabidopsis	826	57	12.4	190	1	PYRE_THETN	P88858 thermomaner
754	57.5	12.5	355	2	Q4JFC3_MOUSE	Q4JFC3 mus musculu	827	57	12.4	228	2	Q83TM7_LISMO	Q83TM7 listeria mo
755	57.5	12.5	356	2	Q9Y941_AERPE	Q9Y941 aeropyrum p	828	57	12.4	230	2	Q8BGA9_SHEON	Q8BGA9 shewanella
756	57.5	12.5	363	2	Q6D013_ERECT	Q6D013 erwinia car	829	57	12.4	241	2	Q658A8_ORYSA	Q658A8 oryza sativ
757	57.5	12.5	371	2	Q53GK2_HUMAN	Q53GK2 homo sapien	830	57	12.4	254	2	Q61095_TRYCR	Q61095 trypanosoma
758	57.5	12.5	371	2	Q9J8C7_9NUCL	Q9J8C7 podopocera	831	57	12.4	258	1	UDP_TREBA	Q83390 treponema p
759	57.5	12.5	374	1	Q8E6_NFYOP	Q8E65 corysila pseu	832	57	12.4	268	2	Q70FH9_9CYAN	Q70FH9 uncultured
760	57.5	12.5	379	1	MCP_CAVPO	P70105 cavia porce	833	57	12.4	269	2	Q8YOW0_ANASP	Q8YOW0 xenopena sp
761	57.5	12.5	383	2	Q8A186_BACTN	Q8A186 bacteroides	834	57	12.4	276	2	Q68BS3_XENLA	Q68BS3 xenopus lae

835	57	12.4	283	2	Q4V7U2_XENLA	Q4V7U2 xenopus lae	908	57	12.4	811	2	Q4FXZ2_LEIMA	Q4fxz2 leishmania
836	57	12.4	291	2	Q5Wx66_LEGPL	Q5wx66 legionella	909	57	12.4	858	2	Q6XPE7_MOUSE	Q6xpe7 mus musculus
837	57	12.4	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	910	57	12.4	880	2	Q6XIO7_MYCMA	Q6xio7 mycoplasma
838	57	12.4	301	2	Q8BYJ2_MOUSE	Q8byj2 mus musculus	911	57	12.4	892	2	Q5LDM6_SILPO	Q5ldm6 silicibacter
839	57	12.4	302	2	Q768S4_MOUSE	Q768s4 mus musculus	912	57	12.4	953	1	FNBR3_MOUSE	FNBR3 mouse
840	57	12.4	315	2	Q9UNE2_HUMAN	Q9une2 homo sapien	913	57	12.4	1056	2	Q5GZ12_XANOR	Q5gz12 xanthomonas
841	57	12.4	325	2	Q9QN99_YVIRU	Q9qn99 rice grassy	914	57	12.4	1137	2	Q8ZB10_STRAW	Q8zbi0 streptomyces
842	57	12.4	332	2	Q5ZM67_PAVLU	Q5zm67 pavlova lut	915	57	12.4	1151	2	Q754S3_ASHGO	Q754s3 ashbya goss
843	57	12.4	334	2	Q5ZM83_BANAT	Q5zm83 bangia atro	916	57	12.4	1294	2	Q5OHM7_STRESH	Q5ohm7 streptomyces
844	57	12.4	342	1	ISIA_STNP7	P15473 synechococc	917	57	12.4	1491	2	Q5GFT1_HAEIN	Q5gft1 haemophilus
845	57	12.4	342	2	Q5N675_SYNP6	Q5n675 synechococc	918	57	12.4	1574	2	Q7Y5J5_9CAUD	Q7y5j5 xanthomonas
846	57	12.4	343	2	Q5LMS6_SILPO	Q5lms6 silicibacter	919	57	12.4	1639	2	Q54J43_DICDI	Q54j43 dictyostell
847	57	12.4	351	2	Q97774_FELCA	Q97774 felis silve	920	57	12.4	1875	2	Q5X8U3_LEGPA	Q5x8u3 legionella
848	57	12.4	352	2	Q867D6_FELCA	Q867d6 felis silve	921	57	12.4	2660	2	Q7Q119_ANOGA	Q7q119 anopheles
849	57	12.4	353	2	Q9LR37_ARATH	Q9lr37 arabidopsis	922	57	12.4	3196	2	Q6ALQ5_DSPPS	Q6alq5 desulfohalob
850	57	12.4	355	2	Q5QNA9_ORYSA	Q5qna9 oryza sativ	923	57	12.4	3338	2	Q8ZPH6_STRAW	Q8zph6 streptomyces
851	57	12.4	355	2	Q8WBK3_YAVES	Q8wbk3 saurothera	924	56.5	12.3	104	2	Q6Z2H4_PSEYM	Q6z2h4 pseudomonas
852	57	12.4	374	2	Q80638_ARATH	Q80638 arabidopsis	925	56.5	12.3	107	2	Q67MA1_SYTWH	Q67ma1 synechobacter
853	57	12.4	374	2	Q9SVF3_ARATH	Q9svf3 arabidopsis	926	56.5	12.3	110	2	Q6J932_9ILIL	Q6j932 xerophyta h
854	57	12.4	374	2	Q67ZB8_ARATH	Q67zb8 arabidopsis	927	56.5	12.3	114	1	HKD3_RAT	HKD3 rat
855	57	12.4	374	2	Q5NWX2_AZOSE	Q5nwx2 azoarcus ap	928	56.5	12.3	120	2	Q6JIA6_HUMAN	Q6jia6 homo sapien
856	57	12.4	376	2	Q6FVJ8_CANGA	Q6fvj8 candida gla	929	56.5	12.3	120	2	Q4MPP5_BACCE	Q4mpps bacillus ce
857	57	12.4	383	2	Q6HGU3_BACHK	Q6hgu3 bacillus th	930	56.5	12.3	120	2	Q6HMB7_BACHK	Q6hmb7 bacillus th
858	57	12.4	383	2	Q81NM9_BACAN	Q81nm9 bacillus an	931	56.5	12.3	120	2	Q631EVS_BAC2	Q631evs bacillus ce
859	57	12.4	384	2	Q65X10_ORYSA	Q65x10 oryza sativ	932	56.5	12.3	143	2	Q81U42_BACAN	Q81u42 bacillus an
860	57	12.4	385	2	Q9SZG0_ARATH	Q9szg0 arabidopsis	933	56.5	12.3	143	2	Q8PLM5_XANAC	Q8plm5 xanthomonas
861	57	12.4	386	2	Q5NFP0_FRATF	Q5nfp0 fransciella	934	56.5	12.3	145	2	Q75ILT0_HUMAN	Q75ilt0 homo sapien
862	57	12.4	387	2	Q5B694_EMENTI	Q5b694 aspergillus	935	56.5	12.3	145	2	Q869G4_LYMST	Q869g4 lymanaea bra
863	57	12.4	387	2	Q6NQC8_DESPS	Q6nqc8 desulfohalob	936	56.5	12.3	148	2	Q9D2U7_MOUSE	Q9d2u7 mus musculus
864	57	12.4	399	2	Q5JU03_SHIFL	Q5ju03 shigella fl	937	56.5	12.3	148	2	Q9J1S0_MOUSE	Q9j1s0 mus musculus
865	57	12.4	409	2	Q639H1_BACC2	Q639h1 bacillus ce	938	56.5	12.3	170	2	Q9W2N2_DROME	Q9w2n2 drosophila
866	57	12.4	425	2	Q4TR85_9SPBN	Q4tr85 erythrobact	939	56.5	12.3	186	2	Q6N191_RHOPA	Q6n191 rhodospheudo
867	57	12.4	440	2	Q9LMU8_ARATH	Q9lm8 arabidopsis	940	56.5	12.3	187	2	Q5Z296_SHIFL	Q5z296 shigella fl
868	57	12.4	440	2	Q8BJG0_MOUSE	Q8bjg0 mus musculus	941	56.5	12.3	187	2	Q7BEL2_SHIFL	Q7bel2 shigella fl
869	57	12.4	456	2	Q97N14_CLOAB	Q97n14 clostridium	942	56.5	12.3	188	2	Q5FRN2_GLUOX	Q5frn2 glucinobacter
870	57	12.4	457	1	PROY_ECOLI	P77329 escherichia	943	56.5	12.3	190	2	Q9JUK1_RAT	Q9juk1 rattus norv
871	57	12.4	457	1	Q83SG9_SHIFL	Q83sg9 shigella fl	944	56.5	12.3	191	2	Q57JF1_SALCH	Q57jf1 salmonella
872	57	12.4	461	1	DCUC_ECOLI	Q47134 escherichia	945	56.5	12.3	191	2	Q5PLD4_SALPA	Q5pld4 salmonella
873	57	12.4	461	2	Q57RUB_SALCH	Q57r8 escherichia	946	56.5	12.3	191	2	Q7CPPO_SALPA	Q7cpo salmonella
874	57	12.4	461	2	Q8FJZ8_ECOL6	Q8fjz8 escherichia	947	56.5	12.3	191	2	Q8XGY6_SALTI	Q8xgy6 salmonella
875	57	12.4	461	2	Q63M54_BURPS	Q63m54 burkholderi	948	56.5	12.3	194	1	TTM22_MOUSE	TTM22 mouse
876	57	12.4	468	2	Q7OD04_ANOGA	Q7od04 anopheles g	949	56.5	12.3	194	2	Q5SSLI_MOUSE	Q5ssli mus musculus
877	57	12.4	471	2	Q5JNBS_ORYSA	Q5jnb5 oryza sativ	950	56.5	12.3	194	2	Q9JUK2_MOUSE	Q9juk2 mus musculus
878	57	12.4	471	2	Q84DP6_LISMO	Q84dp6 listeria mo	951	56.5	12.3	195	2	Q81N78_DROME	Q81n78 drosophila
879	57	12.4	477	2	Q84DP7_LISMO	Q84dp7 listeria mo	952	56.5	12.3	197	2	Q8UOL2_PYRPU	Q8uol2 pyrococcus
880	57	12.4	477	2	Q84DP8_LISMO	Q84dp8 listeria mo	953	56.5	12.3	197	2	Q7JKT6_TREDE	Q7jkt6 treponema d
881	57	12.4	477	2	Q84DP9_LISMO	Q84dp9 listeria mo	954	56.5	12.3	211	2	Q6EST5_FUGRU	Q6est5 fugu rubrip
882	57	12.4	477	2	Q84DQ0_LISMO	Q84dq0 listeria mo	955	56.5	12.3	213	2	Q8NS64_CORGL	Q8ns64 corynebacter
883	57	12.4	477	2	Q83TQ3_LISMO	Q83tq3 listeria mo	956	56.5	12.3	214	2	Q4V6C7_DROME	Q4v6c7 drosophila
884	57	12.4	477	2	Q722W8_LISMF	Q722w8 listeria mo	957	56.5	12.3	228	2	Q84WK4_ARATH	Q84wk4 arabidopsis
885	57	12.4	478	2	Q84DN9_LISMO	Q84dn9 listeria mo	958	56.5	12.3	231	2	Q7UJW2_RHOBA	Q7ujw2 rhodospheudo
886	57	12.4	478	2	Q84DS7_LISMO	Q84ds7 listeria mo	959	56.5	12.3	233	1	LEPX_MYCHO	LEPX mycobacteri
887	57	12.4	487	1	PSBC_FORPU	P51356 porphyra pu	960	56.5	12.3	233	1	LEPX_MYCTU	LEPX mycobacteri
888	57	12.4	487	2	Q8H1D7_ARATH	Q8h1d7 arabidopsis	961	56.5	12.3	234	2	Q92LX9_RHIME	Q92lx9 rhizobium m
889	57	12.4	487	2	Q93ZU2_ARATH	Q93zu2 arabidopsis	962	56.5	12.3	244	2	Q8KZG6_MOUSE	Q8kz6 mus musculus
890	57	12.4	493	2	Q7NCL3_MYCGA	Q7nc13 mycoplasma	963	56.5	12.3	258	2	Q9HP14_HALS4	Q9hp14 halobacteri
891	57	12.4	494	1	ILVC_PHOPE	Q61yz5 photobacter	964	56.5	12.3	274	2	Q4SEPT_TETNG	Q4sept terradodon n
892	57	12.4	517	2	Q88GK6_PSEPK	Q88gk6 pseudomonas	965	56.5	12.3	276	2	Q937L7_9CYAN	Q937l7 uncultured
893	57	12.4	531	2	Q6OVX5_CABER	Q6ovx5 caenorhabdi	966	56.5	12.3	276	2	Q937L8_9CYAN	Q937l8 uncultured
894	57	12.4	534	2	Q4WG10_ASPEFL	Q4wg10 aspergillus	967	56.5	12.3	288	2	Q8Z6Y5_STRAW	Q8z6y5 streptomyces
895	57	12.4	535	2	Q4KIR3_PSEPF	Q4kir3 pseudomonas	968	56.5	12.3	299	2	Q4SGT7_TETNG	Q4sgt7 terradodon n
896	57	12.4	576	2	Q8BYE8_MOUSE	Q8bye8 mus musculus	969	56.5	12.3	304	2	Q4HBA0_9DEIO	Q4hba0 deinochocuss
897	57	12.4	606	2	Q88AM6_PSEBM	Q88am6 pseudomonas	970	56.5	12.3	305	2	Q5ZTIU_CHICK	Q5zt1u gallus gall
898	57	12.4	610	2	Q7Z2H9_HUMAN	Q7z2h9 homo sapien	971	56.5	12.3	335	2	Q8G6M8_BIFLO	Q8g6m8 bifidobacter
899	57	12.4	610	2	Q8N695_HUMAN	Q8n695 homo sapien	972	56.5	12.3	337	1	TH23_TRYBB	TH23 trypanosoma
900	57	12.4	629	2	Q413Y7_GIBZE	Q413y7 gibberella	973	56.5	12.3	337	2	Q9GKES_RABIT	Q9gkes rabbit
901	57	12.4	631	2	Q746H7_THRT2	Q746h7 thermus the	974	56.5	12.3	350	2	Q7UXC7_RHOBA	Q7uxc7 rhodospheudo
902	57	12.4	643	2	Q8MDD4_RABIT	Q8mdd4 erythroclaus	975	56.5	12.3	354	2	Q6ODU9_ORYSA	Q6odu9 oryza sativ
903	57	12.4	643	2	Q6A4I8_BURFI	Q6a4i8 butyrivibrio	976	56.5	12.3	358	2	Q4UKP7_RICPE	Q4ukp7 rickettsia
904	57	12.4	689	2	Q7NIII_GLOVI	Q7niii gleobacter	977	56.5	12.3	364	2	Q4P219_USTMA	Q4p219 ustilago ma
905	57	12.4	705	2	Q4T7V1_TETNG	Q4t7v1 tetradodon n	978	56.5	12.3	368	2	Q5YVAB_NOCFA	Q5yvab nocardia fa
906	57	12.4	792	2	Q4RXC8_TETNG	Q4rxc8 tetradodon n	979	56.5	12.3	372	2	Q5QNB2_ORYSA	Q5qnb2 oryza sativ
907	57	12.4	802	2	Q7UMP8_RHOBA	Q7ump8 rhodospheudo	980	56.5	12.3	374	2	Q517H1_NPVAP	Q517h1 antheraea p

981	56.5	12.3	387	2	Q88L10_PRRPK	Q88I10_pseudomonas	1054	56.5	12.3	758	2	Q811T2_RAT	Q811t2_rattus norv
982	56.5	12.3	391	2	Q6MLC9_BDEBA	Q6mLc9_bdeliovibrio	1055	56.5	12.3	759	2	Q8HXV1_RABIT	Q8hxv1_coryctolagus
983	56.5	12.3	393	2	Q81JG4_BACAN	Q81Jg4_bacillus an	1056	56.5	12.3	769	2	Q81V13_RAT	Q81v13_rattus norv
984	56.5	12.3	394	2	Q7QAA4_ANOGA	Q7qaA4_anopheles g	1057	56.5	12.3	783	2	Q5NXT1_AZOSE	Q5nxt1_azotobacter
985	56.5	12.3	398	2	Q8LRB6_ORYSA	Q8lrb6_oryza sativ	1058	56.5	12.3	852	1	YKML1_YEAST	YKML1_saccharomyc
986	56.5	12.3	403	2	Q7W0P4_BOORP	Q7w0p4_bordetella	1059	56.5	12.3	856	2	Q6G4Z9_BARRH	Q6g4z9_bartonell
987	56.5	12.3	403	2	Q7W3G0_BOORP	Q7w3g0_bordetella	1060	56.5	12.3	889	1	KCNK3_RAT	Q01956_rattus norv
988	56.5	12.3	403	2	Q7W6T0_BOORP	Q7w6t0_bordetella	1061	56.5	12.3	894	2	Q5CNG7_CRYHO	Q5cng7_cryptospori
989	56.5	12.3	407	2	Q4U3Y8_AZOVI	Q4j3y8_azotobacter	1062	56.5	12.3	933	2	Q83GL1_TROWM	Q83gl1_tropheryma
990	56.5	12.3	408	2	Q6LM16_PHOFR	Q6lm16_photobacter	1063	56.5	12.3	939	2	Q5U6I5_HUMAN	Q5u6i5_homo sapien
991	56.5	12.3	409	2	Q6LMI6_PHOFR	Q6lm16_photobacter	1064	56.5	12.3	1000	2	Q5QZ08_IDILLO	Q5qz08_idiomarina
992	56.5	12.3	411	2	Q7P149_CHRYVO	Q7p149_chromobacter	1065	56.5	12.3	1003	2	SEM6A_HUMAN	Q42e08_idiomarina
993	56.5	12.3	414	2	Q4SS40_TENG	Q4ss40_tetradodon n	1066	56.5	12.3	1030	1	Q5P5T6_AZOSE	Q5p5t6_azotobacter
994	56.5	12.3	418	2	Q6UCU9_HUMAN	Q6ucU9_homo sapien	1067	56.5	12.3	1058	2	Q4YP56_PLABE	Q4yp56_plasmodium
995	56.5	12.3	419	1	CARP_CRYPA	P11838_cryptonecter	1068	56.5	12.3	1127	2	Q60RT2_CAEBR	Q60rt2_caenorhabdi
996	56.5	12.3	422	2	Q5PB80_ANAMM	Q5pb80_anaplasma m	1069	56.5	12.3	1241	2	Q4PIV2_TISTMA	Q4piv2_ustilago ma
997	56.5	12.3	428	2	Q5PH29_HUMAN	Q5ph29_homo sapien	1070	56.5	12.3	1250	2	Q4PIV2_TISTMA	Q4piv2_ustilago ma
998	56.5	12.3	442	2	Q5OX17_IDILLO	Q5ox17_idiomarina	1071	56.5	12.3	1643	2	Q5ZCN4_ORYSA	Q5zcn4_oryza sativ
999	56.5	12.3	464	1	NORM_STYNE	Q5mzd9_eynechococ	1072	56.5	12.3	1739	2	Q4SKM5_TETNG	Q4skm5_tetradodon n
1000	56.5	12.3	468	2	Q6JPM6_BURPS	Q6jpm6_burkholderi	1073	56.5	12.3	1778	2	Q414N8_GIBZE	Q414n8_gibberella
1001	56.5	12.3	468	2	Q6ZG62_BURMA	Q6zgg62_burkholderi	1074	56.5	12.3	1838	2	Q6BCJ9_TETTH	Q6bcj9_tetrahymena
1002	56.5	12.3	471	2	Q49635_ARATH	Q49635_arabidopsis	1075	56.5	12.3	1844	2	Q5BDW2_EMENT	Q5bdw2_aspergillus
1003	56.5	12.3	474	2	Q5SMAY_CRYNE	Q5smay_cryptococcu	1076	56.5	12.3	2113	2	Q4RMA1_TETNG	Q4rma1_tetradodon n
1004	56.5	12.3	484	2	Q4ZCK1_9YIRU	Q4zck1_staphylococ	1077	56.5	12.3	2217	2	Q6FMY7_CANGA	Q6fmy7_candida gla
1005	56.5	12.3	484	2	Q4ZCK1_9YIRU	Q4zck1_bacteriopho	1078	56.5	12.3	2876	2	Q4Q8Y3_LEIMA	Q4qbY3_leishmania
1006	56.5	12.3	484	2	Q6GGG4_STPAR	Q6ggg4_staphylococ	1079	56.5	12.3	4464	2	Q7RLJ6_PLAYO	Q7rlj6_plasmodium
1007	56.5	12.3	484	2	Q5HIX6_STPAR	Q5hix6_staphylococ	1080	56.5	12.1	75	2	Q8E590_STRAY	Q8e590_streptococc
1008	56.5	12.3	485	2	Q7CZRT_AGRF5	Q7czrt_agrobacteri	1081	56	12.1	79	1	IVBK1_DENPO	P00981_dendotoxap
1009	56.5	12.3	485	2	Q90YV3_XENIA	Q90yv3_xenopus lae	1082	56	12.1	100	2	Q6N984_RHOPA	Q6n984_rhodospseud
1010	56.5	12.3	491	2	Q4RCUS_USTMA	Q4rcus_ustilago ma	1083	56	12.1	103	1	NIRC_PANDE	Q51702_paracoccu
1011	56.5	12.3	494	2	Q6S12_9PIPT	Q6s612_drosophila	1084	56	12.1	103	2	Q8KZM1_MOUSE	Q8kzm1_mus musculu
1012	56.5	12.3	500	2	Q97KA2_CIOAB	Q97ka2_clostridium	1085	56	12.1	126	2	Q57J16_9BACT	Q57j16_uncultured
1013	56.5	12.3	510	1	Q9RF10_MYXXX	Q9rf10_myxococcus	1086	56	12.1	126	2	Q6J5M4_ECOLI	Q6j5m4_eshcherichia
1014	56.5	12.3	511	1	ZGPAT_MOUSE	Q8vdm1_mus musculu	1087	56	12.1	146	2	Q4NYQ0_9DELT	Q4nyq0_aeromonxyob
1015	56.5	12.3	521	2	Q7RYH0_NEURC	Q7ryh0_neurospora	1088	56	12.1	160	2	Q61T97_CAEBR	Q61t97_caenorhabdi
1016	56.5	12.3	523	2	Q567M6_BRARE	Q567m6_brachydantio	1089	56	12.1	177	2	Q6Z579_GITALA	Q6z579_giardia lam
1017	56.5	12.3	529	1	THA2_TRYBB	Q06222_trypanosoma	1090	56	12.1	177	2	Q7R002_GITALA	Q7r002_giardia lam
1018	56.5	12.3	531	2	Q4UXT1_CONJK	Q4uxT1_corynebacte	1091	56	12.1	196	1	Y286_MYCBE	P47528_mycoplasma
1019	56.5	12.3	567	2	Q4KIT8_PSEFS	Q4kit8_pseudomonas	1092	56	12.1	197	2	Q5FUM6_GLUOX	Q5fum6_glycocalact
1020	56.5	12.3	570	2	Q4WD85_ASPFU	Q4wd85_aspergillus	1093	56	12.1	212	2	Q87MV9_VIBPA	Q87mv9_vibrio para
1021	56.5	12.3	572	2	Q85QSO_9INSE	Q85qso_ritcholepid	1094	56	12.1	218	2	Q9D692_MOUSE	Q9d692_mus musculu
1022	56.5	12.3	595	1	S13AI_HUMAN	Q9hzw2_homo sapien	1095	56	12.1	220	2	Q5LBE4_BACRN	Q5leb4_bacteroides
1023	56.5	12.3	608	2	Q9BAR2_9MAGN	Q9bar2_notobuxus n	1096	56	12.1	222	2	Q9KVF5_VIBCH	Q9kvf5_vibrio chol
1024	56.5	12.3	614	2	Q31615_BACSU	Q31615_bacillus su	1097	56	12.1	228	2	Q5J432_SALCH	Q5j432_salmonella
1025	56.5	12.3	624	2	Q69Z90_MOUSE	Q69z90_mus musculu	1098	56	12.1	230	2	Q5QLP9_ORYSA	Q5qlp9_oryza sativ
1026	56.5	12.3	648	2	Q5EFU5_GLUOX	Q5efu5_glucosinobact	1099	56	12.1	242	2	Q6MEAF_PARUM	Q6meaf_parrachlamyd
1027	56.5	12.3	670	2	Q32212_BACSU	Q32212_bacillus su	1100	56	12.1	249	2	Q5VTM6_BRARE	Q5vtm6_brachydantio
1028	56.5	12.3	681	2	Q9BAO3_9MAGN	Q9baq3_notobuxus a	1101	56	12.1	254	2	Q91207_ONCMY	Q91207_oncorhynch
1029	56.5	12.3	683	2	Q5CVZ7_CRYPV	Q5cvz7_cryptospori	1102	56	12.1	261	2	Q8UAP2_AGRF5	Q8uap2_agrobacteri
1030	56.5	12.3	683	2	Q9BAS3_9MAGN	Q9bas3_buxus micro	1103	56	12.1	264	2	Q9CP61_PASMU	Q9cp61_pasteurella
1031	56.5	12.3	686	1	VGJH_PRIVA	P27416_pseudorabie	1104	56	12.1	274	2	Q4NIS8_9MICC	Q4nis8_athrobacte
1032	56.5	12.3	686	1	VGJH_PRIVA	Q00660_pseudorabie	1105	56	12.1	279	1	Y170_BDCBP	Q89aa2_buchnera ap
1033	56.5	12.3	686	1	VGJH_PRIVA	P27593_pseudorabie	1106	56	12.1	281	2	Q7NUD4_CHRYO	Q7nuD4_chromobacter
1034	56.5	12.3	686	2	Q5PPA2_9ALPH	Q5ppa2_suid herpes	1107	56	12.1	282	2	Q5FI07_LACAC	Q5fi07_lactobacilli
1035	56.5	12.3	688	2	Q9BAS8_9MAGN	Q9bas8_buxus henry	1108	56	12.1	283	2	Q525Q1_MAGGR	Q525q1_magnaporthe
1036	56.5	12.3	689	2	Q7Q3N1_ANOGA	Q7q3n1_anopheles g	1109	56	12.1	286	2	Q9CMW4_PASMU	Q9cmw4_pasteurella
1037	56.5	12.3	690	2	Q9BAS2_9MAGN	Q9baa2_buxus hilde	1110	56	12.1	292	2	Q9U8M8_TACRR	Q9u8m8_lachypleus
1038	56.5	12.3	690	2	Q9BAS4_9MAGN	Q9bas4_buxus ripar	1111	56	12.1	294	2	Q6FRF6_ACTIAD	Q6frf6_actinobact
1039	56.5	12.3	691	2	Q9BAO8_BUXSE	Q9baq8_buxus sempe	1112	56	12.1	295	2	Q7NFB8_GLOVI	Q7nfb8_gloeobacter
1040	56.5	12.3	692	2	Q9BAO9_9MAGN	Q9baq9_buxus likki	1113	56	12.1	302	2	Q7Q9G8_ANOGA	Q7q9g8_anopheles g
1041	56.5	12.3	692	2	Q9BAR0_9MAGN	Q9bar0_buxus gonoc	1114	56	12.1	304	2	Q8ESB3_OCEIH	Q8esb3_oceanobacil
1042	56.5	12.3	692	2	Q9BAS5_9MAGN	Q9bas5_buxus balea	1115	56	12.1	306	2	Q87HY7_VIBPA	Q87hy7_vibrio para
1043	56.5	12.3	692	2	Q9BAS7_9MAGN	Q9bas7_buxus harla	1116	56	12.1	319	2	Q6LIY3_CAEBA	Q6liy3_caenorhabdi
1044	56.5	12.3	695	2	Q9BSW4_HUMAN	Q9bsw4_homo sapien	1117	56	12.1	319	2	Q5O5K1_MOUSE	Q5o5k1_mus musculu
1045	56.5	12.3	699	2	Q9SCT4_BUXSE	Q9sct4_buxus beppe	1118	56	12.1	324	2	Q9P487_TISNU	Q9p487_fischerella
1046	56.5	12.3	704	2	Q9BAS6_9MAGN	Q9bas6_buxus macow	1119	56	12.1	325	2	Q36172_VIVRU	Q36172_rice graaby
1047	56.5	12.3	710	2	Q6C6N0_YARLI	Q6c6n0_yarrowia li	1120	56	12.1	334	2	Q52W82_9RHOD	Q52w82_compopogon
1048	56.5	12.3	710	2	Q8HTM7_PODPE	Q8htm7_podophyllum	1121	56	12.1	340	2	Q5O4U7_HUMAN	Q5o4u7_homo sapien
1049	56.5	12.3	726	2	Q8HTM7_PODPE	Q8htm7_podophyllum	1122	56	12.1	340	2	Q8P9S3_LEPIN	Q8p9s3_leptocyllura
1050	56.5	12.3	726	2	Q8HTM9_9MAGN	Q8htm9_podophyllu	1123	56	12.1	342	2	Q5B7Z1_EMENT	Q5b7z1_aspergillus
1051	56.5	12.3	729	2	Q5PXK6_RAT	Q5pxk6_rattus norv	1124	56	12.1	344	2	Q5AMH7_EMENT	Q5amh7_aspergillus
1052	56.5	12.3	730	2	Q5PXK6_RAT	Q5pxk6_rattus norv	1125	56	12.1	351	2	Q9BEM8_RHILLO	Q9bem8_rhizobium 1
1053	56.5	12.3	757	1	KCNK3_HUMAN	Q14003_homo sapien	1126	56	12.1	352	2	Q6YT41_PIG	Q6yt41_sus scrofa

1127	56	12.1	354	2	06F593_ANAPL	06F593	anas	platyr	1200	56	12.1	568	2	04FXC6_LEIMA	04FXC6	leishmania
1128	56	12.1	359	2	05Z1Y1_NOCFA	05Z1Y1	nocardia	fa	1201	56	12.1	575	2	07N243_PHOIL	07N243	photobabu
1129	56	12.1	361	2	06Z896_ICRPU	06Z896	icrallurus	p	1202	56	12.1	576	2	07N7S6_PHOIL	07N7S6	photobabu
1130	56	12.1	363	2	08BNF7_PSEPK	08BNF7	pseudomonas		1203	56	12.1	578	1	PRF3B_RHOCA	PRF3B	r pte byste
1131	56	12.1	364	2	05U244_HALMA	05U244	haloarcula		1204	56	12.1	581	2	08C3F7_MOUSE	08C3F7	mus musculus
1132	56	12.1	365	2	0981E3_RHLO	0981E3	rhizobium	1	1205	56	12.1	594	2	09X3S5_PSEAB	09X3S5	pseudomonas
1133	56	12.1	376	2	06CNY1_KLUDA	06CNY1	kluyveromyc		1206	56	12.1	605	2	061NM3_XENLA	061NM3	xenopus lae
1134	56	12.1	388	2	09SFX2_ARATH	09SFX2	arabidopsis		1207	56	12.1	610	2	076486_LEIME	076486	leishmania
1135	56	12.1	388	2	0673W2_MOUSE	0673W2	mus musculus		1208	56	12.1	621	2	04PHM6_USTMA	04PHM6	ustilago ma
1136	56	12.1	398	2	07XKE3_ORYSA	07XKE3	oryza sativ		1209	56	12.1	621	2	0660P2_BORGA	0660P2	borrella ga
1137	56	12.1	405	2	07NTU3_CHRYSA	07NTU3	chromobacte		1210	56	12.1	626	2	051574_BORBU	051574	borrella bu
1138	56	12.1	408	2	07PW26_ANOGA	07PW26	anopheles g		1211	56	12.1	629	2	04SUG4_TETNG	04SUG4	tetradon n
1139	56	12.1	409	2	087LM6_VIBPA	087LM6	vibrio para		1212	56	12.1	632	2	09JMA1_CLOPE	09JMA1	clostridium
1140	56	12.1	411	2	09A4V3_CAUCR	09A4V3	caulobacter		1213	56	12.1	638	2	08C415_MOUSE	08C415	mus musculus
1141	56	12.1	413	2	0673T5_SYMTH	0673T5	symbiodacte		1214	56	12.1	643	2	05ON53_ORYSA	05ON53	oryza sativ
1142	56	12.1	434	1	ENO_DESVM	032513	desulfovibr		1215	56	12.1	653	1	KCNH4_HUMAN	KCNH4	human
1143	56	12.1	436	1	ALBD1_BACSU	P71008	bacillus su		1216	56	12.1	690	2	073T97_MYCPA	073T97	mycobacteri
1144	56	12.1	436	1	ALBD2_BACSU	08RTH4	bacillus su		1217	56	12.1	712	2	054Q53_DICDI	054Q53	dictyostell
1145	56	12.1	438	2	09KYG4_STRCO	09KYG4	streptomyce		1218	56	12.1	724	2	08A8Y9_BACTN	08A8Y9	bacteroides
1146	56	12.1	439	2	06BRK2_DEBHA	06BRK2	debaryomyce		1219	56	12.1	736	2	028661_ARCFU	028661	archaeoglob
1147	56	12.1	440	2	08UIZ8_AGRB5	08UIZ8	agrobacteri		1220	56	12.1	752	2	04MY34_9DELT	04MY34	9delet
1148	56	12.1	442	2	0642S2_XENLA	0642S2	xenopus lae		1221	56	12.1	848	2	05RBS4_9HIVI	05RBS4	human
1149	56	12.1	445	2	04HBN0_9DBIO	04HBN0	delnecoccus		1222	56	12.1	855	2	08A6V6_BACTN	08A6V6	bacteroides
1150	56	12.1	449	2	006407_MYCTU	006407	mycobacteri		1223	56	12.1	917	2	04WEX4_ASPFU	04WEX4	aspergillus
1151	56	12.1	449	2	07U1T6_MYCBO	07U1T6	mycobacteri		1224	56	12.1	965	2	05OLFO_9CORY	05OLFO	corynebacte
1152	56	12.1	450	2	06A6T5_PROAC	06A6T5	propionibac		1225	56	12.1	1012	2	07RCG7_PLAYO	07RCG7	plasmidium
1153	56	12.1	452	2	06DOK7_ERACT	06DOK7	erythrina car		1226	56	12.1	1051	2	05ZPD75_ORYSA	05ZPD75	oryza sativ
1154	56	12.1	456	2	084DM6_LISMO	084DM6	liesteria mo		1227	56	12.1	1084	2	05WTH5_LSGPL	05WTH5	legionella
1155	56	12.1	456	2	084DM8_LISMO	084DM8	liesteria mo		1228	56	12.1	1118	2	06BM96_RHIME	06BM96	rhizobium m
1156	56	12.1	456	2	084DM9_LISMO	084DM9	liesteria mo		1229	56	12.1	1118	2	09ZLY97_RHIME	09ZLY97	rhizobium m
1157	56	12.1	457	1	DCR1B_CHICK	05QY13	gallus gall		1230	56	12.1	1126	2	04PEF6_USTMA	04PEF6	ustilago ma
1158	56	12.1	457	2	084DM7_LISMO	084DM7	liesteria mo		1231	56	12.1	1135	2	05X437_LSGPA	05X437	legionella
1159	56	12.1	457	2	084DM7_LISMO	084DM7	liesteria mo		1232	56	12.1	1243	2	04FRM6_9GAMM	04FRM6	9gamm
1160	56	12.1	458	2	084DM5_LISMO	084DM5	liesteria mo		1233	56	12.1	1305	1	FTECK_YERPE	FTECK	yerpe
1161	56	12.1	458	2	084DM6_LISMO	084DM6	liesteria mo		1234	56	12.1	1310	2	066CR2_YERPS	066CR2	yerps
1162	56	12.1	459	2	05FML2_XENLA	05FML2	xenopus lae		1235	56	12.1	1384	1	CNRP1_HUMAN	CNRP1	human
1163	56	12.1	461	2	084DQ5_LISMO	084DQ5	liesteria mo		1236	56	12.1	1406	2	06LJG4_SOLDE	06LJG4	solanum dem
1164	56	12.1	461	2	06ZD13_BURMA	06ZD13	burkholderi		1237	56	12.1	1439	2	07XQPI_ORYSA	07XQPI	oryza sativ
1165	56	12.1	471	2	084DQ3_LISMO	084DQ3	liesteria mo		1238	56	12.1	1462	2	081IWO_PLAF7	081IWO	plasmidium
1166	56	12.1	477	2	084DM5_LISMO	084DM5	liesteria mo		1239	56	12.1	1520	2	05SUB6_CRYNS	05SUB6	cryptococcu
1167	56	12.1	477	2	084DM0_LISMO	084DM0	liesteria mo		1240	56	12.1	1608	2	05Y9LO_HUMAN	05Y9LO	human
1168	56	12.1	477	2	084DM1_LISMO	084DM1	liesteria mo		1241	56	12.1	1856	1	GBF1_CRIGR	GBF1	crigri
1169	56	12.1	477	2	084DM3_LISMO	084DM3	liesteria mo		1242	56	12.1	1859	1	GBF1_HUMAN	GBF1	human
1170	56	12.1	478	2	084DPO_LISMO	084DPO	liesteria mo		1243	56	12.1	1875	2	06RCQ2_LSGPN	06RCQ2	legionella
1171	56	12.1	479	2	084DP3_LISMO	084DP3	liesteria mo		1244	56	12.1	1875	2	05Z276_LSGPH	05Z276	legionella
1172	56	12.1	480	2	05Z2N7_MACGR	05Z2N7	magnaporthe		1245	56	12.1	1914	1	RUF_HUMAN	RUF	human
1173	56	12.1	488	2	04NEK3_9M1CC	04NEK3	arctrobacte		1246	56	12.1	1914	1	05RCL4_PONPY	05RCL4	pongy
1174	56	12.1	490	2	07N3C6_PHOIL	07N3C6	photobabu		1247	56	12.1	2055	1	MPDZ_MOUSE	MPDZ	mouse
1175	56	12.1	494	2	05V4M5_HALMA	05V4M5	haloarcula		1248	56	12.1	1972	2	07PMJ6_ANOGA	07PMJ6	anoga
1176	56	12.1	503	1	VLI_HPV32	P36737	human papil		1249	56	12.1	6994	2	017343_CABEL	017343	cabel
1177	56	12.1	503	1	05N5S0_SYNPS	05N5S0	synecbococ		1250	56	12.1	6994	2	017490_CABEL	017490	cabel
1178	56	12.1	508	2	08FP11_CORNF	08FP11	corynebacte		1251	55.5	12.0	62	2	08CKT3_YERPE	08CKT3	yerpe
1179	56	12.1	516	2	08CE47_MOUSE	08CE47	mus musculu		1252	55.5	12.0	63	2	04FLU9_9RICK	04FLU9	9rick
1180	56	12.1	516	2	094M77_CTEFR	094M77	ctenogobio		1253	55.5	12.0	84	2	05WGD8_BACSK	05WGD8	bacsk
1181	56	12.1	518	2	04IHP5_GIBZE	04IHP5	gibberella		1254	55.5	12.0	124	2	08BLJ31_PSEPK	08BLJ31	psepk
1182	56	12.1	519	2	09VXK1_DROME	09VXK1	drosophila		1255	55.5	12.0	134	2	06RSR7_BACCE	06RSR7	bacce
1183	56	12.1	524	2	081R66_BACCR	081R66	baclillus ce		1256	55.5	12.0	138	2	05TLI8_MOUSE	05TLI8	mouse
1184	56	12.1	525	2	04R8B0_TETNG	04R8B0	tetradon n		1257	55.5	12.0	141	2	06YXR7_PHYPA	06YXR7	phycomitrite
1185	56	12.1	528	2	04KCT5_PSEPF	04KCT5	pseudomonas		1258	55.5	12.0	147	2	063K49_BURPS	063K49	burps
1186	56	12.1	531	2	041973_GIBZE	041973	gibberella		1259	55.5	12.0	147	2	06ZB21_BURMA	06ZB21	burkholderi
1187	56	12.1	531	2	CH60_EYTAG	066500	enterobacte		1260	55.5	12.0	151	2	08BDH7_VIBVO	08BDH7	vibrio vuln
1188	56	12.1	539	1	CH60_KURTAS	066190	enterobacte		1261	55.5	12.0	157	2	093287_BROIN	093287	bromus iner
1189	56	12.1	540	1	CH60_KLEFOR	066210	klebsiella		1262	55.5	12.0	168	2	06U398_LACPL	06U398	lactobacilli
1190	56	12.1	540	1	CH60_KLEFOX	066210	klebsiella		1263	55.5	12.0	177	2	04LXV9_9BURK	04LXV9	9burkholderi
1191	56	12.1	544	1	CH60_AERSA	068309	aeromonas s		1264	55.5	12.0	179	2	06LME1_PROPR	06LME1	photobacter
1192	56	12.1	545	2	06TLJ7_9PSEBD	06TLJ7	pseudomonas		1265	55.5	12.0	184	2	07BKF5_PROB01	07BKF5	gamma-prote
1193	56	12.1	547	1	CH60_KLEPM	066026	klebsiella		1266	55.5	12.0	186	2	08JUM5_SHIFL	08JUM5	shigella fl
1194	56	12.1	547	2	09Z2B8_RHIME	09Z2B8	rhizobium m		1267	55.5	12.0	186	2	05W7KO_XENTR	05W7KO	xenopus tro
1195	56	12.1	548	2	06YXJ3_XENNE	06YXJ3	xenorhabdus		1268	55.5	12.0	187	2	0707B6_ECOLI	0707B6	escherichia
1196	56	12.1	557	1	PMO4_HUMAN	P31512	homo sapien		1269	55.5	12.0	187	2	08CVQ9_ECOLI	08CVQ9	escherichia
1197	56	12.1	557	1	Q5RDN6_PONPY	Q5rdn6	pongy pygma		1270	55.5	12.0	191	2	06E5S2_FUGRU	06E5S2	fugu rubrip
1198	56	12.1	558	2	053XR0_HUMAN	Q53XR0	homo sapien		1271	55.5	12.0	194	1	TM22_HUMAN	TM22	human
1199	56	12.1	559	2	06UN75_TOBAC	Q6un75	nicotiana t		1272	55.5	12.0	196	1	CLEP1_PROMP	CLEP1	promchloroco

1273	55.5	12.0	198	2	Q87A07_XYLFT	Q87A07_xylletia fas	1346	55.5	12.0	382	2	Q5B1F0_BOVIN	Q5b1f0_bos taurus
1274	55.5	12.0	199	2	Q65D47_BACLD	Q65d47_bacillus l1	1347	55.5	12.0	383	1	YJUK8_YEAST	P2946_saccharomyc
1275	55.5	12.0	206	2	Q95E77_BRAOL	Q95e77_braessica ol	1348	55.5	12.0	383	2	Q6Q5N7_YEAST	Q6q5n7_saccharomyc
1276	55.5	12.0	211	2	Q9NA02_9CRUS	Q9na02_daphnia mag	1349	55.5	12.0	383	2	Q5Z0K5_NOCFA	Q5z0k5_nocardia fa
1277	55.5	12.0	213	2	Q9NA09_CABEL	Q9na09_caenorhabdi	1350	55.5	12.0	384	2	Q9L1J8_BRANA	Q9l1j8_braessica fa
1278	55.5	12.0	214	2	Q61ZM4_CABER	Q61zm4_caenorhabdi	1351	55.5	12.0	384	2	Q9L1A9_ARATH	Q9l1a9_arabidopsis
1279	55.5	12.0	221	2	Q6CLJ3_KULUA	Q6clj3_kluyveromyc	1352	55.5	12.0	385	2	Q9FX15_ARATH	Q9fx15_arabidopsis
1280	55.5	12.0	223	2	Q9DCP4_MOUSE	Q9dcp4_mus musculu	1353	55.5	12.0	385	2	Q6PQJ8_DIGPU	Q6pqj8_diglyphalis p
1281	55.5	12.0	232	2	Q8B5R5_9TOMB	Q8b5r5_beet black	1354	55.5	12.0	389	2	Q5HVJ0_CAMJR	Q5hvj0_campylobact
1282	55.5	12.0	235	2	Q4LOA6_9BURK	Q4loa6_burkholderi	1355	55.5	12.0	389	2	Q9PPF7_CAMJR	Q9ppf7_campylobact
1283	55.5	12.0	237	2	Q419H8_G1BZE	Q419h8_glibberella	1356	55.5	12.0	393	2	Q4NMJ1_9DELT	Q4nmj1_aeromonycob
1284	55.5	12.0	237	2	Q4Z0A9_PSESY	Q4z0a9_pseudomonas	1357	55.5	12.0	394	2	Q560G3_CRYNE	Q560g3_cryptococcu
1285	55.5	12.0	237	2	Q8B5Y3_PSEBSM	Q8b5y3_pseudomonas	1358	55.5	12.0	407	2	Q947C6_TRIMO	Q947c6_triticum mo
1286	55.5	12.0	240	2	Q8XW05_RALSO	Q8xw05_ralstonia s	1359	55.5	12.0	409	2	Q4NRD2_9DELT	Q4nrd2_aeromonycob
1287	55.5	12.0	245	2	Q9B8R9_MYCPU	Q9b8r9_mycoplasma	1360	55.5	12.0	414	2	Q7MNR0_V1BIV	Q7mnr0_vibrio vuln
1288	55.5	12.0	245	2	Q7ZYW1_BARRI	Q7zyw1_brachydantio	1361	55.5	12.0	417	2	Q9Z1S3_ECOLI	Q9z1s3_escherichia
1289	55.5	12.0	248	2	Q6CA49_YARLI	Q6ca49_yarrowia li	1362	55.5	12.0	425	2	Q5WRV3_LEGGL	Q5wrv3_legionella
1290	55.5	12.0	250	2	Q8B147_BRARJ	Q8b147_bradyrhicob	1363	55.5	12.0	425	2	Q5WXT6_LEGGL	Q5wxt6_legionella
1291	55.5	12.0	253	2	Q7PJ20_ANOGS	Q7pj20_amopheles g	1364	55.5	12.0	425	2	Q5X6C6_LEGPA	Q5x6c6_legionella
1292	55.5	12.0	253	2	Q8FPB6_COREF	Q8fpb6_corynebacte	1365	55.5	12.0	431	2	Q9MS90_9MAGN	Q9ms90_austroballe
1293	55.5	12.0	254	2	Q9RWPI_DEIRA	Q9rwp1_deinococcus	1366	55.5	12.0	437	2	Q83CB5_COXBU	Q83cb5_coxiella bu
1294	55.5	12.0	256	2	Q9RUK4_DEIRA	Q9ruk4_deinococcus	1367	55.5	12.0	451	2	Q4NMW3_9DELT	Q4nmw3_aeromonycob
1295	55.5	12.0	257	1	PEBB_PROMM	Q7585_prochloroxo	1368	55.5	12.0	452	2	Q8KAS7_CHLRE	Q8kas7_chlorobium
1296	55.5	12.0	262	1	BACR_HALSA	P02945_halobacteri	1369	55.5	12.0	456	2	Q205J3_CABEL	Q205j3_caenorhabdi
1297	55.5	12.0	262	2	Q5HLT2_STAEQ	Q5hl12_staphylococ	1370	55.5	12.0	459	2	Q9C1K1_LACLA	Q9c1k1_lactococcus
1298	55.5	12.0	262	2	Q4G5W6_BRARE	Q4g5w6_brachydantio	1371	55.5	12.0	470	2	Q7MSR1_WOLSV	Q7msr1_wollinella s
1299	55.5	12.0	263	2	Q5CVY7_CRYPR	Q5cvy7_cryptospori	1372	55.5	12.0	471	2	Q5FTZ0_GLUOX	Q5ftz0_glucosylact
1300	55.5	12.0	263	2	Q5CFK0_CRYHO	Q5cfk0_cryptospori	1373	55.5	12.0	483	2	Q91BZ9_ONCMW	Q91b29_oncorhynch
1301	55.5	12.0	270	2	Q5VUJ0_HUMAN	Q5vu10_homo sapien	1374	55.5	12.0	484	2	Q4ZCR7_9VIRU	Q4zcr7_bacteriophu
1302	55.5	12.0	270	2	Q9B866_HALMA	Q9b866_brachydantio	1375	55.5	12.0	484	2	Q7JRS3_TREDE	Q7jrs3_trepionema d
1303	55.5	12.0	283	2	Q5V2V1_HALMA	Q5v2v1_haloarctua	1376	55.5	12.0	484	2	Q8NWL7_STAMW	Q8nwl7_staphylococ
1304	55.5	12.0	292	2	Q91XR2_CAVPO	Q91xr2_cavia porce	1377	55.5	12.0	516	2	Q5JBB0_9LILI	Q5jbb0_toxicoscord
1305	55.5	12.0	295	2	Q6GNN7_XENLA	Q6gnn7_xenopus lae	1378	55.5	12.0	522	2	Q8D5G2_V1BIV	Q8d5g2_vibrio vuln
1306	55.5	12.0	299	2	Q9H218_PSEAB	Q9h218_pseudomonas	1379	55.5	12.0	522	2	Q7MCQ9_V1BIV	Q7mcq9_vibrio vuln
1307	55.5	12.0	300	2	Q5P7J6_AZOSB	Q5p7j6_azarcus sp	1380	55.5	12.0	528	2	Q73K08_TREDE	Q73k08_trepionema d
1308	55.5	12.0	309	2	Q8DPP1_STRR6	Q8dpp1_streptococc	1381	55.5	12.0	528	2	Q4RJ06_TRENG	Q4rj06_tetradonema n
1309	55.5	12.0	309	2	Q97QL2_STRPN	Q97ql2_streptococc	1382	55.5	12.0	529	2	Q5CP72_CRYHO	Q5cp72_cryptospori
1310	55.5	12.0	312	1	CATO_MOUSE	Q8bm88_mus musculu	1383	55.5	12.0	545	2	Q8PYL8_ANASP	Q8pyl8_anabeana sp
1311	55.5	12.0	312	1	Q4QQL3_MOUSE	Q4qq13_mus musculu	1384	55.5	12.0	545	2	Q9PXA4_9PARA	Q9pxa4_measles vir
1312	55.5	12.0	315	2	Q6LHU3_PHOPR	Q6lhu3_photobacter	1385	55.5	12.0	546	2	Q91HA5_9PARA	Q91ha5_reindeer
1313	55.5	12.0	316	2	Q9RUA8_DEIRA	Q9rua8_deinococcus	1386	55.5	12.0	553	2	Q11B80_9PARA	Q11b80_measles vir
1314	55.5	12.0	317	1	EXOZ_RHIME	P25502_rhizobium m	1387	55.5	12.0	562	1	Y3471_BRARJ	Q89p29_bradyrhicob
1315	55.5	12.0	323	2	Q888H6_PSEBSM	Q888h6_pseudomonas	1388	55.5	12.0	566	2	Q5H4R5_XANOR	Q5h4r5_xanthomonas
1316	55.5	12.0	324	2	Q9BF59_ATEFU	Q9bf59_ateles fusc	1389	55.5	12.0	572	2	Q5R773_PONPY	Q5r773_pongo pygma
1317	55.5	12.0	325	2	Q6LGS8_PHOPR	Q6lgs8_photobacter	1390	55.5	12.0	580	2	Q9BDA6_RHIL0	Q9bda6_rhizobium l
1318	55.5	12.0	326	2	Q97CS8_THIEVO	Q97cs8_thermoplasma	1391	55.5	12.0	587	2	Q9FKO5_ARATH	Q9fk05_arabidopsis
1319	55.5	12.0	326	2	Q9BFA8_PIG	Q9bfa8_sus scrofa	1392	55.5	12.0	595	2	Q5RSH6_PONPY	Q5rs16_pongo pygma
1320	55.5	12.0	326	2	Q9BFF0_LEMCA	Q9bff0_lemur catta	1393	55.5	12.0	596	2	Q7NJB4_GLOVI	Q7njb4_gloeobacter
1321	55.5	12.0	326	2	Q9BFF2_SORAR	Q9bff2_sorex arane	1394	55.5	12.0	607	2	Q9CY11_ARATH	Q9cy11_arabidopsis
1322	55.5	12.0	326	2	Q9BF75_MYRTR	Q9bf75_myrmecophag	1395	55.5	12.0	625	1	KCNCA4_RAT	Q63734_rattus norv
1323	55.5	12.0	326	2	Q9BF76_TAMTE	Q9bf76_tamandua te	1396	55.5	12.0	628	1	KCNCA4_MOUSE	Q63740_mus musculu
1324	55.5	12.0	326	2	Q99N07_AGOTA	Q99nq7_agouti tacz	1397	55.5	12.0	631	2	Q7VND5_HABDU	Q7vnd5_haemophilus
1325	55.5	12.0	326	2	Q99N09_HYDHY	Q99n09_hydrochoeru	1398	55.5	12.0	631	2	Q803A6_BRARE	Q803a6_brachydantio
1326	55.5	12.0	326	2	Q99NR0_9HYST	Q99nr0_cavia tachu	1399	55.5	12.0	634	2	Q961J0_DROME	Q961j0_drosophila
1327	55.5	12.0	326	2	Q99NR3_EREDO	Q99nr3_erechizon d	1400	55.5	12.0	643	1	KCNCA4_HUMAN	Q93720_homo sapien
1328	55.5	12.0	326	2	Q99NR4_HYSBR	Q99nr4_hysetrix bra	1401	55.5	12.0	643	1	YKDE_CABEL	Q03564_caenorhabdi
1329	55.5	12.0	326	2	Q99NR8_CASCN	Q99nr8_casstor cana	1402	55.5	12.0	648	1	PRIA_RICPR	Q92d10_rickettsia
1330	55.5	12.0	331	2	Q59NG1_CANAL	Q59ng1_candida alb	1403	55.5	12.0	662	1	HEPA_HHVEU	P52375_human herpes
1331	55.5	12.0	331	2	Q5KPK4_CRYNE	Q5kpk4_cryptococcu	1404	55.5	12.0	678	2	Q82F42_STRAM	Q82f42_streptococc
1332	55.5	12.0	336	2	Q4H4M1_9DEIO	Q4h4m1_deinococcus	1405	55.5	12.0	687	2	Q9BXR6_HUMAN	Q9bxr6_homo sapien
1333	55.5	12.0	341	2	Q4H4Z8_9DEIO	Q4h4z8_deinococcus	1406	55.5	12.0	698	2	Q84Z10_ORYSA	Q84z10_oryza sativ
1334	55.5	12.0	343	2	Q98865_BRARE	Q98865_brachydantio	1407	55.5	12.0	716	1	P5CS_ORYSA	Q04226_o_delta 1-p
1335	55.5	12.0	344	2	Q8YQJ5_ANASP	Q8yqj5_anabaena sp	1408	55.5	12.0	716	1	Q6PW76_ORYSA	Q6pw76_oryza sativ
1336	55.5	12.0	346	2	Q59293_PYRHO	Q59293_pyrococcus	1409	55.5	12.0	716	2	Q60EM4_ORYSA	Q60em4_oryza sativ
1337	55.5	12.0	346	2	Q740N5_MYCPA	Q740n5_mycobacteri	1410	55.5	12.0	726	2	Q8HTM8_9MAGN	Q8htm8_diphylleia
1338	55.5	12.0	357	2	Q8Q1TC_STYVAH	Q8q1tc_adoxophyes	1411	55.5	12.0	740	2	Q8DUI7_SYNTL	Q8dji7_erythrococc
1339	55.5	12.0	358	2	Q67TC7_SYNTM	Q67tc7_symbiodacte	1412	55.5	12.0	742	2	Q6MNV6_BDEBA	Q6mnv6_bdellovibri
1340	55.5	12.0	376	1	OE56_NPVAC	P41705_autographa	1413	55.5	12.0	751	2	Q9AYM4_VIGUN	Q9aym4_vigna ungui
1341	55.5	12.0	378	1	Q8B9B5_NPVRO	Q8b9b5_rachiplusia	1414	55.5	12.0	788	2	Q6INE9_XENLA	Q6ine9_xenopus lae
1342	55.5	12.0	379	1	OE56_NPVCF	P41718_choristoneu	1415	55.5	12.0	806	1	PAZG6_HUMAN	Q60733_homo sapien
1343	55.5	12.0	379	2	Q8B2F2_PSEBSM	Q8b2f2_pseudomonas	1416	55.5	12.0	806	2	Q7MWJ0_BORRA	Q7mwj0_bordetella
1344	55.5	12.0	379	2	Q77DF6_NPVCF	Q77df6_choristoneu	1417	55.5	12.0	806	2	Q7MPJ0_BORBR	Q7mpj0_bordetella
1345	55.5	12.0	381	2	Q8ZB18_STRAM	Q8zb18_streptomyce	1418	55.5	12.0	806	2	Q7MPJ0_V1BIV	Q7mpj0_vibrio vuln


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1419 55.5 12.0 849 2 QARGD7 TETNG
1420 55.5 12.0 880 2 QAKM12 BRARE
1421 55.5 12.0 886 1 SEM6B MOUSE
1422 55.5 12.0 887 1 SEM6B_RAT
1423 55.5 12.0 888 1 SEM6B_HUMAN
1424 55.5 12.0 893 1 DAG1_MOUSE
1425 55.5 12.0 893 2 Q8BPJ7 MOUSE
1426 55.5 12.0 893 2 Q8CB66 MOUSE
1427 55.5 12.0 893 2 Q544G5 MOUSE
1428 55.5 12.0 895 1 DAG1_BOVIN
1429 55.5 12.0 925 1 Q7XPE9 ORYSA
1430 55.5 12.0 946 1 C1TC_YEAST
1431 55.5 12.0 968 2 Q8TW58 METKA
1432 55.5 12.0 1020 2 Q95XY4 CAEBEL
1433 55.5 12.0 1062 2 Q7OV26 GIALA
1434 55.5 12.0 1104 2 Q7S728 NEUCR
1435 55.5 12.0 1119 2 Q5BA79 EMENI
1436 55.5 12.0 1131 2 Q6C011 YARLI
1437 55.5 12.0 1148 2 Q54YC9 DICDI
1438 55.5 12.0 1217 2 Q17889 CAEBEL
1439 55.5 12.0 1423 1 FRUA_STRMU
1440 55.5 12.0 1453 2 Q7F6T3 9CORA
1441 55.5 12.0 1469 2 Q4WTA3 ASPFU
1442 55.5 12.0 1632 2 Q5SID3 TETNG
1443 55.5 12.0 1637 2 Q5O297 ENTHI
1444 55.5 12.0 1731 2 Q4OJ23 LEIMA
1445 55.5 12.0 1913 2 Q4Q986 LEIMA
1446 55.5 12.0 2054 1 MPD2_RAT
1447 55.5 12.0 2220 2 Q9GV40 DROME
1448 55.5 12.0 2236 2 Q9VCN1 DROME
1449 55.5 12.0 4805 2 Q4FE23 LEIMA
1450 55.5 11.9 52 2 Q45059 CAEBEL
1451 55.5 11.9 66 2 Q7UB93 SYNXP
1452 55.5 11.9 92 2 Q4RYG8 TETNG
1453 55.5 11.9 93 2 Q82Q38 STRAW
1454 55.5 11.9 94 2 Q85P51 9CUCU
1455 55.5 11.9 95 2 Q864R3 CANFA
1456 55.5 11.9 123 2 Q6LGG8 PHCPA
1457 55.5 11.9 128 1 Y070_TREPA
1458 55.5 11.9 134 2 Q86ZV1 NEUCR
1459 55.5 11.9 159 2 Q5XDS9 STRP6
1460 55.5 11.9 159 2 Q9A0V4 STRP6
1461 55.5 11.9 159 2 Q7CNF4 STRP8
1462 55.5 11.9 159 2 Q7CPB9 STRP3
1463 55.5 11.9 160 1 P8TD_GDTH
1464 55.5 11.9 166 2 Q5Q8S5 PHATP
1465 55.5 11.9 178 1 CRCB2_BIFLO
1466 55.5 11.9 190 2 Q6W3A0 9CREN
1467 55.5 11.9 202 2 Q62XV1 BURMA
1468 55.5 11.9 208 2 Q63TK1 BURPS
1469 55.5 11.9 208 2 Q9PSA1 CHICK
1470 55.5 11.9 212 2 Q8B874 VIBVU
1471 55.5 11.9 212 2 Q9KGG3 VIBCH
1472 55.5 11.9 218 2 Q848N7 9BACT
1473 55.5 11.9 220 2 Q841E1 BACFR
1474 55.5 11.9 223 2 Q9XCA4 PORGI
1475 55.5 11.9 225 2 Q9BRQ7 HUMAN
1476 55.5 11.9 228 2 Q83Y73 LISMO
1477 55.5 11.9 228 2 Q63R53 BURPS
1478 55.5 11.9 229 2 Q62HE2 BURMA
1479 55.5 11.9 229 2 Q83TM3 LISMO
1480 55.5 11.9 229 2 Q83UH3 LISMO
1481 55.5 11.9 235 2 Q8NC40 HUMAN
1482 55.5 11.9 235 2 Q7MM99 VIBVU
1483 55.5 11.9 242 2 Q9BSV0 HUMAN
1484 55.5 11.9 252 2 Q61UV0 PODAN
1485 55.5 11.9 252 2 Q7TNC3 MOUSE
1486 55.5 11.9 253 2 Q631Q1 BURPS
1487 55.5 11.9 255 2 Q8TUS5 METKA
1488 55.5 11.9 263 2 Q8GFE8 STRAU
1489 55.5 11.9 263 2 Q79ND6_FRAIT
1490 55.5 11.9 264 2 Q6Z3B6 ORYSA
1491 55.5 11.9 265 2 Q7PIL4_CHRVO

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Q4RGD7 tetraodon n
Q4KM12 brachydanio
Q54951 mus musculus
Q70141 rattus norv
Q91313 homo sapien
Q62165 mus musculu
Q8BPJ7 mus musculu
Q8CB66 mus musculu
Q544G5 mus musculu
Q18738 bos taurus
Q7XPE9 oryza sativ
P07245 s c-1-tetra
Q8TW58 mechanopyru
Q95XY4 caenorhabdi
Q7GV26 giardia lam
Q7S728 neurospora
Q5BA79 aspergillus
Q6C011 yarrowia li
Q54YC9 dictyosteli
Q17889 caenorhabdi
Q03174 streptococc
Q7F6T3 canine coro
Q4WTA3 aspergillus
Q4SID3 tetraodon n
Q5O297 entamoeba h
Q4OJ23 leishmania
Q4Q986 leishmania
Q55164 rattus norv
Q9GV40 dirosophila
Q9VCN1 drosophila
Q4FE23 leishmania
Q45059 caenorhabdi
Q7UB93 synecchococ
Q4RYG8 tetraodon n
Q82Q38 streptomyc
Q85P51 oclorhynchu
Q864R3 canis famli
Q6LGG8 photobacter
Q83109 treponema p
Q86ZV1 neuropept
Q5XDS9 streptococ
Q9A0V4 streptococ
Q7CNF4 streptococ
Q7CPB9 streptococ
Q7S728 guillardia
Q5Q8S5 phaeogale
Q8GFE8 bitidobacte
Q6W3A0 uncultured
Q62XV1 burkholderi
Q63TK1 burkholderi
Q9PSA1 gallus gall
Q8B874 vibrio vuln
Q9KGG3 vibrio chol
Q848N7 uncultured
Q841E1 bacteroides
Q9XCA4 porphyromon
Q9BRQ7 homo sapien
Q83Y73 listeria mo
Q63R53 burkholderi
Q62HE2 burkholderi
Q83TM3 listeria mo
Q83UH3 listeria mo
Q8NC40 homo sapien
Q7MM99 vibrio vuln
Q9BSV0 homo sapien
Q61UV0 podospira a
Q7TNC3 mus musculu
Q631Q1 burkholderi
Q8TUS5 metanopyru
Q8GFE8 streptomyc
Q79ND6 francisella
Q6Z3B6 oryza sativ
Q7PIL4 chromobacte

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1492 55 11.9 268 1 EA30_VICFA
1493 55 11.9 268 2 Q43675 VICFA
1494 55 11.9 270 2 Q94006 CANAL
1495 55 11.9 270 2 Q5A4M8 CANAL
1496 55 11.9 270 2 Q8BY38 MOUSE
1497 55 11.9 273 2 Q73NN2 TREDE
1498 55 11.9 275 2 Q54KD4 DICDI
1499 55 11.9 277 2 Q9FEY3 ARATH
1500 55 11.9 282 2 Q9Y4U1_HUMAN

ALIGNMENTS

Q6UWZ1_HUMAN PRELIMINARY; PRT; 89 AA.
ID Q6UWZ1_HUMAN PRELIMINARY; PRT; 89 AA.
AC Q6UWZ1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ERVY526
GN Name=ERVY4; ORFNames=UNQ526;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975109; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie B., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmon L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yamanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358584; AA088947.1; -, mRNA.
DR HGNC; HGNC:4028; ERVY4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; P:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000272; FXYD.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXYD; 1.
SQ
SEQUENCE 89 AA; 9433 MW; CS9342818244980 CRC64;

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 3e-41;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLGLTALRANRPFANKDDPFYYDMKNLQISGLICGGLIATIAIAVLSGK 60
DB 1 MERVTLALLLGLTALRANRPFANKDDPFYYDMKNLQISGLICGGLIATIAIAVLSGK 60

QY 61 CKYKSSQKHSPVPEKAIPLTPGSAATTC 89
DB 61 CKYKSSQKHSPVPEKAIPLTPGSAATTC 89

RESULT 2
Q74W5_HUMAN PRELIMINARY; PRT; 89 AA.
ID Q74W5_HUMAN PRELIMINARY; PRT; 89 AA.
AC Q74W5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

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DT 13-SEP-2005 (TrEMBL:rel. 31, last annotation update)
DE FXID domain containing ion transport regulator 4.
GN Name=FXID; ORFNames=Rpl1-92P6.2-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RA Straube R.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP Corby N.;
RA Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC054876; AAH54876.1; -; mRNA.
DR EMBL; AL512654; CA117065.1; -; genomic_DNA.
DR Ensembl; ENSG00000150201; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000272; FXID.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXID; 1.
SQ SEQUENCE 89 AA; 9373 MW; C595929A2449B0 CRC64;
Query Match 98.0%; Score 452; DB 2; Length 89;
Best local similarity 98.9%; Pred. No. 2.7e-40;
Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MERVTLALLLGLTALFANDPANKDDPFYDMKNLQSLGICGLAIAVAVSGK 60
DB 1 MERVTLALLLGLTALFANDPANKDDPFYDMKNLQSLGICGLAIAVAVSGK 60
QY 61 CKYSSQKQHSVPVEKAIPLITPGSATTC 89
DB 61 CKYSSQKQHSVPVEKAIPLITPGSATTC 89
RESULT 3
FXID_HUMAN STANDARD; PRT; 89 AA.
AC P53646;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FXID domain-containing ion transport regulator 4 precursor.

GN Name=FXID;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RT "The FXID gene family of small ion transport regulators or channels:
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the FXID family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; A182935; -; NOT ANNOTATED CDS; mRNA.
CC Ensembl; ENSG00000150201; Homo sapiens.
DR HGN; HGNC:4028; FXID.
DR InterPro; IPR00272; FXID.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXID; 1.
KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
FT SIGNAL 1 20
FT CHAIN 21 89
FT TOPO_DOM 21 38
FT TRANSMEM 39 59
FT TOPO_DOM 60 89
SQ SEQUENCE 89 AA; 9373 MW; B595EP9A9449B4 CRC64;
Query Match 97.6%; Score 450; DB 1; Length 89;
Best local similarity 97.8%; Pred. No. 4.5e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MERVTLALLLGLTALFANDPANKDDPFYDMKNLQSLGICGLAIAVAVSGK 60
DB 1 MERVTLALLLGLTALFANDPANKDDPFYDMKNLQSLGICGLAIAVAVSGK 60
QY 61 CKYSSQKQHSVPVEKAIPLITPGSATTC 89
DB 61 CKYSSQKQHSVPVEKAIPLITPGSATTC 89

RESULT 4
 FXPD4 MOUSE STANDARD; PRT; 88 AA.
 ID FXPD4 MOUSE
 AC Q9D2M7
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXPD domain-containing ion transport regulator 4 precursor (Channel inducing factor) (CHIF).
 GN Name=Fxpd4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CX [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=129/SvJ;
 RA Garty H.;
 RT "Genomic sequence of mouse CHIF (FXPD4).";
 RU Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nishida I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Choctha C., Corbali L.E., Cousins S., Dalla E., Dregan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D., Kawai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kongsang A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A., Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.J., Perlea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandell A., Schneider C., Sempke C.A., Seton M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hitzane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shitaki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Struhsberg R.L., Felting E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins B.S., Wagner L., Shemen C.M., Schler G.D., Altshul S.F., Zeeberg S., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullihy S.J., Bosa S.S., Loguigliano N.A., Peters G.J., Abiraman R.D., Mullihy S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Murthy D.W., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodighiero S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Kizyewski M.I., Skalska U., Smailus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 CC CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the Fxpd family.
 CC
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: AF362729; AAK51508.1; -; Genomic_DNA.
 CC EMBL: AK018728; BAB31372.1; -; mRNA.
 CC EMBL: BC086918; AAB86918.1; -; mRNA.
 CC EMBL: ENSMUSG0000004988; Mus musculus.
 CC MGI: MGI:189005; Fxpd4.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0016021; C:integral to membrane; TAS.
 CC InterPro: IPR000272; Fxpd
 CC Pfam: PF02038; ATP1C1_PLM_MAT8; 1.
 CC PROSITE: PS01310; Fxpd; 1.
 CC Ion transport; Ionic channel; Signal; Transmembrane; Transport.
 CC SIGNAL
 CC CHAIN 1 20 Potential.
 CC FT 21 88 Fxpd domain-containing ion transport
 CC FT TOPO DOM 39 59 regulator 4.
 CC FT TOPO DOM 60 88 Extracellular (Potential).
 CC FT SEQUENCE 88 AA; 9269 MW; 7EB0140941CFE926 CRC64;
 Query Match 60.0%; Score 276.5; DB 1; Length 88;
 Best Local Similarity 66.7%; Pred. No. 1.4e-21;
 Matches 60; Conservative 8; Mismatches 19; Indels 3; Gaps 3;
 Oy 1 MERVLA-LLLLAGTALFANPDPPYDKNTQLSGLLCGMLAIAVAVSG 59
 Db 1 MEIRICALLLLAGPALFASDP-VKDSFFYDWSIQGLIRGGLCTAGIMALSG 59
 Oy 60 KCKYKSSQKSHSPVEKAIPLTPGSARTC 89
 Db 60 KCKCRTHKP-SLPGKATPLIPGSANTC 88
 RESULT 5
 FXPD4 RAT STANDARD; PRT; 87 AA.
 ID FXPD4 RAT
 AC Q63113;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXPD domain-containing ion transport regulator 4 precursor (Channel inducing factor) (CHIF) (Corticosteroid-induced protein).
 GN Name=Fxpd4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Wistar; TISSUE=Colon;
 RX MEDLINE=95320221; PubMed=7597086;
 RA Attali B., Latier H., Rachamin N., Garty H.;
 RT "A corticosteroid-induced gene expressing an 'Isk-like' K+ channel activity in Xenopus oocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:6092-6096(1995).
 [2]
 RN TISSUE SPECIFICITY.
 RP MEDLINE=9700648; PubMed=8843704;
 RX Caputo C., Couty N., Bonvalet J.-P., Becoubet B., Garty H.,

RA Farman N.;
 RT "Cellular localization and regulation of CHIF in kidney and colon.";
 RL Am. J. Physiol. 271:C753-C762(1996).
 CC -1- FUNCTION: Induces a potassium channel when expressed in Xenopus oocytes.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Selectively present in the distal parts of the nephron (medullary and papillary collecting ducts and end portions of cortical collecting tubule) and in the epithelial cells of the distal colon. No expression is found in renal proximal tubule, loop of henle and distal tubule, proximal colon, small intestine, lung, choroid plexus, salivary glands, or brain.
 CC -1- INDUCTION: By corticosteroids.
 CC -1- SIMILARITY: Belongs to the FXVD family.
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 CC EMBL: L41254; AAA74691.1; -; mRNA.
 DR PIR: I59391; I59391.
 DR Ensembl: ENSRM00000014578; Rattus norvegicus.
 DR RGD: 70998; Fxyd4.
 DR GO: GO:0005267; F:potassium channel activity; IDA.
 DR InterPro: IPR000272; FXVD.
 DR Pfam: PF02038; ATP1g1_PLM_MAT8; 1.
 DR PROSITE: PS01310; ATP1g1_PLM_MAT8; 1.
 KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 1 87 FXVD domain-containing ion transport
 FT FT regulator 4.
 FT TOPO_DOM 21 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 87 Cytoplasmic (Potential).
 SQ SEQUENCE 87 AA; 9084 MW; 5D0D1FPC6B1BCA CRC64;
 Query Match 55.6%; Score 256.5; DB 1; Length 87;
 Best Local Similarity 61.5%; Pred. No. 1.9e-19;
 Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;
 QY 1 MERTLA-LLLAGTAEANDPPANKDDPPYDKMQLQSLGCGLLAAGIAVSG 59
 DB 1 MEGTICAFGLVLAGLPVEANGP-VDKSPFYDWESLQGLMGICIAIAMLG 59
 QY 60 KCKYSSOKOSP--VPEKAPLITPGSATT 88
 DB 60 KCK--CRNHTPSLPEKVTPLITPGSAST 87
 RESULT 6
 FXVD MOUSE STANDARD; PRT; 88 AA.
 AC Q61835;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXVD domain-containing ion transport regulator 3 precursor (Chloride conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein) (Phospholemman-like).
 DE Name=Fxyd3; Synonyms=Mat8, Plm1;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RX NCBI [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=95060797; PubMed=7970700;
 RA Morrison B.W.; Leder P.;
 RT "neu and ras initiate murine mammary tumors that share genetic markers

RT generally absent in c-myc and int-2-initiated tumors.";
 RL Oncogene 9:3417-3426(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin A.A., Hong L.,
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko V., Boulfard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Smalhe U.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP EXPRESSION.
 RX MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;
 RA Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
 RA Leder P.;
 RT "Mat-8, a novel phospholemman-like protein expressed in human breast tumors, induces a chloride conductance in Xenopus oocytes.";
 RL J. Biol. Chem. 270:2176-2182(1995).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current when expressed in Xenopus oocytes. May be a modulator capable of activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in a subset of murine breast tumors.
 CC -1- MISCELLANEOUS: Marker of a cell type preferentially transformed by neu or ras oncoprotein.
 CC -1- SIMILARITY: Belongs to the FXVD family.
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 CC EMBL: X93038; CAAG3606.1; -; mRNA.
 DR EMBL: BC002039; AA020209.1; -; mRNA.
 DR EMBL: BC056223; AA056223.1; -; mRNA.
 DR PIR: S61552; S61552.
 DR Ensembl: ENSMUSG00000057092; Mus musculus.
 DR MGI: MGI:107497; Fxyd3.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR InterPro: IPR000272; FXVD.
 DR Pfam: PF02038; ATP1g1_PLM_MAT8; 1.
 DR PROSITE: PS01310; FXVD; 1.
 KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
 KW Transmembrane; Transport.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 1 88 FXVD domain-containing ion transport
 FT FT regulator 3.
 FT TOPO_DOM 21 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 88 Cytoplasmic (Potential).
 SQ SEQUENCE 88 AA; 9526 MW; 9CD61684B856E35D CRC64;
 Query Match 52.4%; Score 241.5; DB 1; Length 88;
 Best Local Similarity 57.8%; Pred. No. 7.5e-18;
 Matches 52; Conservative 11; Mismatches 24; Indels 3; Gaps 3;

QY 1 MERVTLALL-LLAGTALBANDPANKDDPFYDMKQLQSLGICGLIAGIAVLSG 59
 DB 1 MGEVLSLVLVLGLPTLNDAMP-ENKDPFYDMWLSLVGGLICGLIAGIIVLSG 59
 QY 60 KCKYKSSQKOHSPVPEKAIPLITPGSATTG 89
 DB 60 KCKCKFRQKP-SHREPGDPPPLITPGSAHNC 88

RESULT 7
 ID FXD3_RAT STANDARD; PRT; 88 AA.
 AC P59645;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 3 precursor.
 OS Name=FXD3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OK NCBI_TaxId=10116;
 RN NUCLEOTIDE SEQUENCE.
 RP Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J.,
 RA Kerlavage A.R., Adams M.D., EMBL/GenBank/DBJ databases.
 RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.
 RX RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
 RA MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
 RA Swadlow K.J., Rael E.;
 RT "The FXD gene family of small ion transport regulators or channels:
 RT CDNA sequence, protein signature sequence, and expression.";
 RL Genomics 68:41-56(2000).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May be a modulator capable of
 CC activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the FXD family.
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AA013165; -; NOT ANNOTATED CDS; mRNA.
 DR Ensemble; ENSRNOG0000021095; Rattus norvegicus.
 DR InterPro; IPR000272; FXD.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE; PS01310; FXD; 1.
 KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 88 FXD domain-containing ion transport
 FT regulator 3.
 FT TOPO_DOM 21 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 88 Cytoplasmic (Potential).
 SQ SEQUENCE 88 AA; 9411 MW; 45AFB872FDIAF944 CRC64;

Query Match 50.9%; Score 234.5; DB 1; Length 88;
 Best Local Similarity 56.7%; Pred. No. 4,2e-17;
 Matches 51; Conservative 10; Mismatches 26; Indels 3; Gaps 3;

RESULT 8
 ID FXD3_PIG STANDARD; PRT; 88 AA.
 AC O97797;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 3 precursor (Chloride
 DE conductance inducer protein Mac-8) (Mammary tumor 8 KDa protein).
 OS Name=FXD3; Synonyms=Mat8;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OK NCBI_TaxId=9823;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=gastric mucosa;
 RX MEDLINE=99140476; PubMed=10206733;
 RA Maeda M., Hamano K., Hirano Y., Suzuki M., Takahashi E.-I., Terada T.,
 RA Futai M., Sato R.;
 RT "Structures of P-type transporting ATPases and chromosomal locations
 RT of their genes.";
 RL Cell Struct. Funct. 23:315-323(1998).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May be a modulator capable of
 CC activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the FXD family.
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 CC removed.
 CC -----
 CC EMBL, AB015759; BA035078.1; -; mRNA.
 DR InterPro; IPR000272; FXD.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE; PS01310; FXD; 1.
 KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
 KW Transmembrane; Transport.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 88 FXD domain-containing ion transport
 FT regulator 3.
 FT TOPO_DOM 18 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 88 Cytoplasmic (Potential).
 SQ SEQUENCE 88 AA; 9314 MW; 6CC7810B90512E5A CRC64;

Query Match 50.0%; Score 230.5; DB 1; Length 88;
 Best Local Similarity 57.8%; Pred. No. 1.1e-16;
 Matches 52; Conservative 10; Mismatches 25; Indels 3; Gaps 3;

RESULT 9
 ID FXD3_HUMAN STANDARD; PRT; 87 AA.
 AC Q14802; Q13211;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 3 precursor (Chloride

DE conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
 GN (Phospholemman-like).
 OS Name=FXVD3; Synonyms=Mat8, PLML;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 CC Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RX MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;
 RA Morrison B.W., Moorman J.R., Kowaley G.C., Kobayashi Y.M., Jones L.R.,
 RA Leder P.;
 RT "Mat-8, a novel phospholemman-like protein expressed in human breast
 RT tumors, induces a chloride conductance in Xenopus oocytes.";
 RL J. Biol. Chem. 270:2176-2182 (1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung carcinoma;
 RA Lei W., Wu M.;
 RN Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schin J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May be a modulator capable of
 CC activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in a subset of human breast tumors.
 CC -1- MISCELLANEOUS: Marker of a cell type preferentially transformed by
 CC neu or ras oncoprotein.
 CC -1- SIMILARITY: Belongs to the FXVD family.
 CC
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 CC removed.
 CC -----
 CC EMBL, X93036; CAA63604.1; -; mRNA.
 CC EMBL, U28249; AAA73922.1; -; mRNA.
 CC EMBL, BC005238; AAH05238.1; -; mRNA.
 CC PIR, A55571; A55571.
 CC Ensemble: ENSG00000089356; Homo sapiens.
 CC HGNC, HGNC:4027; FXVD3.
 CC H-InvDB, HIX0018290; -.
 CC MIM, 604996; -.
 CC GO, GO:0005887; C:integral to plasma membrane; TAS.
 CC GO, GO:0005254; P:chloride channel activity; TAS.
 CC GO, GO:0006821; P:chloride transport; TAS.
 CC InterPro, IPR000272; FXVD.

DR Pfam, PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE, PS01310; FXVD; 1.
 KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
 KW Transmembrane; Transport.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 87 FXVD domain-containing ion transport
 FT FT regulator 3.
 FT TOPO_DOM 21 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 87 Cytoplasmic (Potential).
 FT CONFLICT 35 37 Missing (in Ref. 2).
 FT CONFLICT 58 58 S->SEMRSSGEAGRGKSPPLTTQLSPNG (in Ref.
 FT FT 2).
 SQ SEQUENCE 87 AA; 9263 MW; 6D674D668EB32493 CRC64;
 Query Match 46.5%; Score 214.5; DB 1; Length 87;
 Best Local Similarity 54.5%; Pred. No. 5.6e-15;
 Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;
 QY 1 MERVTLALL-LAGLTALLEANPPANDDPYYDMKNLQLSGILGILAIAGIAVLSG 59
 DB 1 MQRVTGLGLVFLAGFVPLDAND-LEDKNSPFYDMHSLQVGGLICAGVLCAMGIIVWSA 59
 QY 60 KCKTKSSOKQ-HSPVPEKAIPITPGSA 86
 DB 60 KCKCKFGQKSGHH--PGETPLITPGSA 85
 RESULT 10
 G61B59 HUMAN
 ID G61B59_HUMAN PRELIMINARY; PRT; 87 AA.
 AC G61B59;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE FXVD3 protein (FXVD domain containing ion transport regulator 3,
 DE isoform 1).
 GN Name=FXVD3;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 CC Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., Labaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Mkundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
 RT vector.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=White Matter pool - 5 brain tissues - femoral artery;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.
 RG NIH MGC Project;
 RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL, CR456945; CAG33226.1; -; mRNA.
 DR EMBL, CR542197; CAG46994.1; -; mRNA.
 DR EMBL, BT006712; AAP35358.1; -; mRNA.
 DR EMBL, BC090044; AAH90044.1; -; mRNA.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0005216; P:ion channel activity; IEA.
 DR GO, GO:0006811; P:ion transport; IEA.
 DR InterPro, IPR000272; FYXD.
 DR Pfam, PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE, PS01310; FYXD; 1.
 SQ SEQUENCE 87 AA; 9263 MW; 6D674D66EB32493 CRC64;

Query Match 46.5%; Score 214.5; DB 2; Length 87;
 Best Local Similarity 54.5%; Pred. No. 5,6e-15;
 Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

Oy 1 MERVTLALL-LLAGLTALANDPFAKDDPFYDWMKQLSLGICGLAIAAGIAVSG 59
 Db 1 MQKVTLGLVFLAGPVLIDAND-LEDKNSPFYDWSLQVGLICAGVLCAGIIVMSA 59
 60 KCKKSSOKO-HSPVPEKAIPLITPSA 86
 Db 60 KCKKFGKSGSHH--PGETPPLITPSA 85

RESULT 11
 080UV3 MOUSE PRELIMINARY; PRT; 70 AA.
 ID 080UV3_MOUSE PRELIMINARY; PRT; 70 AA.
 AC 080UV3_MOUSE PRELIMINARY; PRT; 70 AA.
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE FYXD3 protein.
 GN Name=FYXD3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Kleinberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schler G.D.,
 RA Kleinberg R.L., Collins F.S., Wagner L., Schemm C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A., Rubin G.M., Hong L.,
 RA Stajich M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothyluk S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.
 RG NIH MGC Project;
 RL Submitted (APR-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC051033; AAH51033.1; -; mRNA.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0005216; P:ion channel activity; IEA.
 DR GO, GO:0006811; P:ion transport; IEA.
 DR InterPro, IPR000272; FYXD.
 DR Pfam, PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE, PS01310; FYXD; 1.
 SQ SEQUENCE 70 AA; 7773 MW; AB2A5EAF1490BF08 CRC64;

Query Match 44.0%; Score 203; DB 2; Length 70;
 Best Local Similarity 59.4%; Pred. No. 7,6e-14;
 Matches 41; Conservative 10; Mismatches 16; Indels 2; Gaps 2;

Oy 1 MERVTLALL-LLAGLTALANDPFAKDDPFYDWMKQLSLGICGLAIAAGIAVSG 59
 Db 1 MQKVTLGLVFLAGPVLIDAND-LEDKNSPFYDWSLQVGLICAGVLCAGIIVMSA 59
 60 KCKKSSOK 68
 Db 60 KCKKFGKSGSHH--PGETPPLITPSA 85

RESULT 12
 PLM_HUMAN STANDARD; PRT; 92 AA.
 ID PLM_HUMAN STANDARD; PRT; 92 AA.
 AC 000168;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Phospholemmann precursor (FYXD domain-containing ion transport
 DE regulator 1).
 GN Name=FYXD1; Synonyms=PLM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=97312702; PubMed=9169143; DOI=10.1006/geno.1997.4665;
 RA Chen L.-S.K., Lo C.F., Numann R., Cuddy M.,
 RA "Characterization of the human and rat phospholemmann (PLM) cDNAs and
 RT localization of the human PLM gene to chromosome 19q13.1";
 RT Genomics 41:435-443(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
 RA Sweedner K.J., Reel E.,
 RA "The FYXD gene family of small ion transport regulators or channels:
 RT cDNA sequence, protein signature sequence, and expression.";
 RN Genomics 68:41-56(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain, Lung, and Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rane S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,
RA Villalón D.K., Mzany D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
CC when expressed in *Xenopus* oocytes. May have a functional role in
CC muscle contraction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highest expression in skeletal muscle and
CC heart. Moderate levels in brain, placenta, lung, liver, pancreas,
CC uterus, bladder, prostate, small intestine and colon with mucosal
CC lining. Very low levels in kidney, colon and small intestine
CC without mucosa, prostate without endothelial lining, spleen, and
CC testis.
CC -1- PM: Major plasma membrane substrate for cAMP-dependent protein
CC kinase (PK-A) and protein kinase C (PK-C) in several different
CC tissues (by similarity). Phosphorylated in response to insulin and
CC adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the FYXD family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: U72345; AAC51286.1; -; mRNA.
CC EMBL: BC032800; AAH32800.1; -; mRNA.
CC Ensembl: ENSG00000126258; Homo sapiens.
CC HGNC: HGNC:4025; FXYP1.
CC MIM: 602359; -;
CC GO: GO:0005887; C: integral to plasma membrane; TAS.
CC GO: GO:0005886; C: plasma membrane; TAS.
CC GO: GO:0005254; F: chloride channel activity; TAS.
CC GO: GO:0006821; F: chloride transport; TAS.
CC GO: GO:0006936; P: muscle contraction; TAS.
CC InterPro: IPR000272; FYXD.
CC Pfam: PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE: PS01110; FYXD_1.
CC Chloride, Chloride channel, Ion transport, Ionic channel,
CC Phosphorylation, Signal, Transmembrane, Transport.
CC SIGNAL 1 20 By similarity.
CC CHAIN 21 92 Phospholeman.
CC FT TOPO_DOM 21 35 Extracellular (Potential).
CC FT TRANSMEM 36 56 Potential.
CC FT TOPO_DOM 57 92 Cytoplasmic (Potential).
CC FT MOD_RES 83 83 Phosphoserine (by PKA and PKC).
CC FT MOD_RES 88 88 Phosphoserine (by PKA and PKC).
CC FT CONFLICT 3 3 S -> P (in Ref. 1).
CC FT CONFLICT 5 5 G -> H (in Ref. 1).
CC FT CONFLICT 92 92 AA; 10441 MW; 11602EFAFPD8D8 CRC64;
CC
CC Query Match 28.0%; Score 129; DB 1; Length 92;
CC Best Local Similarity 41.3%; Pred. No. 7.8e-06;
CC Matches 26; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

Db 15 LTMKASP--KEHDPFYDQSLGGLVIGLILVLSRCKPNOQORTGE 72
Oy 74 PEK 76
Db 73 PDE 75

RESULT 13
O4RF62 TERNG PRELIMINARY; PRT; 88 AA.
ID O4RF62 TERNG PRELIMINARY; PRT; 88 AA.
AC O4RF62;
DT 13-SEP-2005 (TRENBERL 31, Last sequence update)
DT 13-SEP-2005 (TRENBERL 31, Last sequence update)
DE Chromosome 8 SCAFI5119, whole genome shotgun sequence.
GN ORNames=GSTENG0003534001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salenibat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellil V., Katika M., Vacherie B.,
RA Blomont C., Skalli Z., Catalicio L., Poulain J., De Berardinis V.,
RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Querier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RA "Genome duplication in the teleost fish *Tetraodon nigriviridis* reveals
RA the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL: CAAB0105119; CAG12870.1; -; Genomic DNA.
CC SO SEQUENCE 88 AA; 9614 MW; 7067B3ED3574AA13 CRC64;

CC Query Match 27.7%; Score 127.5; DB 2; Length 88;
CC Best Local Similarity 43.3%; Pred. No. 1.1e-05;
CC Matches 29; Conservative 13; Mismatches 20; Indels 5; Gaps 2;

Oy 5 TLALL--LAGTRLEANDPFPYDQSLGGLVIGLILVLSRCK 62
Db 4 TCALLMTLTLAAAEHSP--EDPFTDHRHLRVGLIILVLSRCK 60
Oy 63 YKSQK 69
Db 61 CKRNQK 67

RESULT 14
ID PLM CANFA STANDARD; PRT; 92 AA.
AC P66513;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phospholeman precursor (FYXD domain-containing ion transport
DE regulator 1)
GN Name=FYXD; Synonyms=PLM;
OS Canis familiaris (Dog).

Search completed: December 14, 2005, 06:34:13
Job time : 234 secs
